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OM nucleic - nucleic search, using sw model

Run on: September 2, 2004, 13:12:03; Search time 103 Seconds
(without alignments)
6513.938 Million cell updates/sec

Title: US-10-087-080-31

Perfect score: 1209
Sequence: 1 atgaagcttgagagctgtcgtt.....tggagagctcctcctagcttga 1209

Scoring table: OLIGO NUC
Gapco 60.0, Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	6.6	320	4	US-09-833-381-1266
2	25	2.1	1965	2	US-09-220-133-21
3	25	2.1	4695	2	US-08-231-193A-57
4	25	2.1	4695	2	US-08-486-273A-57
5	25	2.1	4695	2	US-08-940-086A-57
6	25	2.1	4695	4	US-08-940-035A-57
7	25	2.1	4695	4	US-08-935-105A-57
8	25	2.1	4695	4	US-09-648-797-57
9	25	2.1	4695	4	US-09-386-123-57
10	24	2.0	159	3	US-09-437-457-11
11	24	2.0	429	4	US-09-641-638-324
12	24	2.0	1860	2	US-08-331-644-3
13	24	2.0	1860	5	PCT-US93-04102-3
14	24	2.0	3387	1	US-08-064-271-11
15	24	2.0	3387	2	US-08-627-254C-29
16	24	2.0	3387	4	US-09-023-655-1050
17	22	1.8	3387	4	US-08-930-589A-19
18	22	1.8	3387	4	US-09-599-781-19
19	20	1.7	480	4	US-09-674-608A-4
20	20	1.7	1454	4	US-09-372-422A-19
21	20	1.7	2561	4	US-09-616-289-48
22	20	1.7	4403765	3	US-09-103-840A-2
23	20	1.7	441529	3	US-09-103-840A-1
24	19	1.6	576	4	US-09-252-991A-13112
25	19	1.6	633	4	US-09-252-991A-12687
26	19	1.6	720	4	US-09-252-991A-2351
27	19	1.6	720	4	US-09-252-991A-2640

c	28	19	1.6	1101	4	US-09-489-039A-2638	Sequence 2638, Ap
c	29	19	1.6	1192	3	US-09-318-448-18	Sequence 18, Ap
c	30	19	1.6	1248	4	US-09-489-039A-6144	Sequence 6144, Ap
c	31	19	1.6	1278	4	US-09-252-991A-2483	Sequence 2483, Ap
c	32	19	1.6	1563	4	US-09-252-991A-2566	Sequence 2566, Ap
c	33	19	1.6	2124	4	US-09-252-991A-12830	Sequence 12830, A
c	34	19	1.6	2634	3	US-08-941-936-1	Sequence 1, Appl
c	35	19	1.6	3623	1	US-08-306-691B-35	Sequence 35, Appl
c	36	19	1.6	43280	2	US-08-804-227C-1	Sequence 1, Appl
c	37	18	1.5	18	2	US-08-627-254C-12	Sequence 12, Appl
c	38	18	1.5	248	4	US-09-397-787-24	Sequence 24, Appl
c	39	18	1.5	420	4	US-09-252-991A-7967	Sequence 7967, Ap
c	40	18	1.5	504	4	US-09-252-991A-9584	Sequence 9584, Ap
c	41	18	1.5	957	4	US-09-252-991A-51	Sequence 51, Appl
c	42	18	1.5	1077	4	US-09-522-714-17	Sequence 17, Appl
c	43	18	1.5	1143	4	US-09-252-991A-5748	Sequence 5748, Ap
c	44	18	1.5	1188	4	US-09-252-991A-5131	Sequence 5131, Ap
c	45	18	1.5	1239	4	US-09-252-991A-9666	Sequence 9666, Ap

ALIGNMENTS

```
RESULT 1
US-09-833-381-1266
; Sequence 1266, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1266
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(320)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1266

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-24;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 567 GGACAACTAGTGGATGCTCAACCCCAAGAGGATACCTTGGCGAGGGGCTCTCG 626
Db 1 GGACAACTAGTGGATGCTCAACCCCAAGAGGATACCTTGGCGAGGGGCTCTCG 60

QY 627 CCGCCGCCGCAAGCGCTCA 646
Db 61 CCGCCGCCGCAAGCGCTCA 80

RESULT 2
US-09-220-132-21
; Sequence 21, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1996-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
```

PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 1965
TYPE: DNA
ORGANISM: Homo sapiens
US-09-220-132-21

Query Match 2.1%; Score 25; DB 4; Length 1965;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 CCTACTCGTACATCGGCTCATCG 382
Db 196 CCTACTCGTACATCGGCTCATCG 220

RESULT 3

US-08-231-193A-57
Sequence 57, Application US/08231193A
Patent No. 5849895
GENERAL INFORMATION:
APPLICANT: Daggett, Lorie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: U.S.A.
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,193A
FILING DATE: 20-APR-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9383
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 4695 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 485..4495
US-08-231-193A-57

Query Match 2.1%; Score 25; DB 2; Length 4695;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGGCGGCGGCGGCGG 309
Db 3700 GGGGCCAGGCGGCGGCGGCGG 3724

RESULT 4

US-08-486-273A-57
Sequence 57, Application US/08486273A
Patent No. 5985586
GENERAL INFORMATION:
APPLICANT: Daggett, Lorie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA
TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: U.S.A.
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,273A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9383B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 4695 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 485..4495
US-08-486-273A-57

Query Match 2.1%; Score 25; DB 2; Length 4695;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGGCGGCGGCGGCGG 309
Db 3700 GGGGCCAGGCGGCGGCGGCGG 3724

RESULT 5

US-08-940-086A-57
Sequence 57, Application US/08940086A
Patent No. 6111091
GENERAL INFORMATION:
APPLICANT: Daggett, Lorie P.
APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,086A
FILING DATE: 29-SEPT-97
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9383C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 450-8499
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 4695 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 485..4495
US-08-940-086A-57

Query Match 2.1%; Score 25; DB 3; Length 4695;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGCGCGCGCGCGCGCGG 309
DB 3700 GGGGCCAGCGCGCGCGCGCGCGG 3724

RESULT 6
US-08-940-035A-57
Sequence 57, Application US/08940035A
Patent No. 6316611
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.

ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,035A
FILING DATE: 29-SEPT-97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9383E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 4695 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 485..4495
US-08-940-035A-57

Query Match 2.1%; Score 25; DB 4; Length 4695;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGCGCGCGCGCGCGCGG 309
DB 3700 GGGGCCAGCGCGCGCGCGCGCGG 3724

RESULT 7
US-08-935-105A-57
Sequence 57, Application US/08935105A
Patent No. 6376660
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,105A
FILING DATE: 29-SEPT-97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9383D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 4695 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 485..4495
US-08-935-105A-57

Query Match 2.1%; Score 25; DB 4; Length 4695;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGGGCGGGCGGGCGGGG 309
Db 3700 GGGGCCAGGGCGGGCGGGCGGGG 3724

RESULT 8
US-09-648-797-57
Sequence 57, Application US/09648797
Patent No. 6469142
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
Ellis, Steven B.
Liew, Chen W.
Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehtman White & McAniff
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/648,797
FILING DATE: 28-Aug-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/940,086A
FILING DATE: 29-SEPT-97
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 2435-9383C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 450-8499
INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 4695 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 485..4495
US-09-648-797-57

Query Match 2.1%; Score 25; DB 4; Length 4695;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGGGCGGGCGGGCGGGG 309
Db 3700 GGGGCCAGGGCGGGCGGGCGGGG 3724

RESULT 9
US-09-386-123-57
Sequence 57, Application US/09386123
Patent No. 6521413
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
Ellis, Steven B.
Liew, Chen W.
Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehtman White & McAniff
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/386,123
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,273
FILING DATE: 06-JUNE-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9383F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 4695 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:

Query Match 2.0%; Score 24; DB 2; Length 1860;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 CCTACTCGTACATCGCGCTCATC 381
Db 759 CCTACTCGTACATCGCGCTCATC 782

RESULT 13
PCT-US93-04102-3
; Sequence 3, Application PC/TUS9304102
; GENERAL INFORMATION:
; APPLICANT: Tao, Wufan
; APPLICANT: Lai, Eseng
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04102
; FILING DATE: 19930430
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,292
; FILING DATE: 13-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41472A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; TRLEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1860 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US93-04102-3

Query Match 2.0%; Score 24; DB 5; Length 1860;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 CCTACTCGTACATCGCGCTCATC 381
Db 759 CCTACTCGTACATCGCGCTCATC 782

RESULT 14
US-08-064-271-11
; Sequence 11, Application US/08064271
; Patent No. 5543297
; GENERAL INFORMATION:
; APPLICANT: Kennedy, Brian P.
; APPLICANT: Cromlish, Manda A.
; APPLICANT: Mancini, Joseph A.
; APPLICANT: O'Neill, Gary
; APPLICANT: Vickers, Philip J.

APPLICANT: Wong, Elizabeth
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 cDNA AND
; TITLE OF INVENTION: ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in, 1.4Kb
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,271
; FILING DATE: 19930506
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Panzer, Curtis C.
; REGISTRATION NUMBER: 33,752
; REFERENCE/DOCKET NUMBER: 189061A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3199
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3387 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-064-271-11

Query Match 2.0%; Score 24; DB 1; Length 3387;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 890 GCGCGGCGCCCTGCGCGCGCTGC 913
Db 73 GCGCGGCGCCCTGCGCGCGCTGC 96

RESULT 15
US-08-627-254C-29
; Sequence 29, Application US/08627254C
; Patent No. 5859229
; GENERAL INFORMATION:
; APPLICANT: Kniss, Douglas A.
; TITLE OF INVENTION: Eicosanoid Formation
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griwold LLP
; STREET: 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,254C
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Golick, Mary E.
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 18525/00107

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8200
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-627-254C-29

Query Match 2.0%; Score 24; DB 2; Length 3387;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 890 GGCGCGCGCGCTGCGCGCGCTGC 913
Db 73 GGCGCGCGCGCTGCGCGCGCTGC 96

Search completed: September 2, 2004, 15:11:14
Job time : 106 secs

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QY 181 GGGGACGGGGAAGAGTGGGGAGGGGCGGGGCGGGAGAGGAGATCCCGGACGA 240
 Db 181 GGGGACGGGGAAGAGTGGGGAGGGGCGGGGCGGGAGAGGAGATCCCGGACGA 240
 QY 241 GGTGCTGACAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 300
 Db 241 GGTGCTGACAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 300
 QY 301 GGGGCGGGGAGGGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 Db 301 GGGGCGGGGAGGGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 QY 361 TACTGCTGACATGCGGCTCATGCGATGCGGATGCGGATGCGGATGCGGATGCGG 420
 Db 361 TACTGCTGACATGCGGCTCATGCGATGCGGATGCGGATGCGGATGCGGATGCGG 420
 QY 421 CTGGCGGAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCA 480
 Db 421 CTGGCGGAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCA 480
 QY 481 GGTGCTGACAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 540
 Db 481 GGTGCTGACAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 540
 QY 541 GGGGACGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 600
 Db 541 GGGGACGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 600
 QY 601 TACAGCTTGGGCGGAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 660
 Db 601 TACAGCTTGGGCGGAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 660
 QY 661 GTTCCCGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 720
 Db 661 GTTCCCGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 720
 QY 721 GGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 780
 Db 721 GGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 780
 QY 781 AGCGCGGCGGAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 840
 Db 781 AGCGCGGCGGAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 840
 QY 841 GCGGACGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 900
 Db 841 GCGGACGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 900
 QY 901 TGGCGGCGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 960
 Db 901 TGGCGGCGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 960
 QY 961 CCGGCTGCGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 1020
 Db 961 CCGGCTGCGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 1020
 QY 1021 CCGGCTGCGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 1080
 Db 1021 CCGGCTGCGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 1080
 QY 1081 CTGCGGAGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 1140
 Db 1081 CTGCGGAGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 1140
 QY 1141 CTGCGGAGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 1200
 Db 1141 CTGCGGAGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 1200
 QY 1201 CTAGCTTGA 1209
 Db 1201 CTAGCTTGA 1209

RESULT 2
 US-10-274-177-9
 ; Sequence 9, Application US/10274177
 ; Publication No. US20040038225A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARKOWITZ, Sanford D.
 ; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
 ; FILE REFERENCE: CWRU-P01-003
 ; CURRENT APPLICATION NUMBER: US/10/274,177
 ; CURRENT FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: US/10/229,345
 ; PRIOR FILING DATE: 2002-08-26
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 1209
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1161)..(1161)
 ; OTHER INFORMATION: n=a, c, g, or t
 ; US-10-274-177-9
 Query Match 100.0%; Score 1209; DB 13; Length 1209;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGTTGAGGAGTGTTCCTGCTCGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 60
 Db 1 ATGAGTTGAGGAGTGTTCCTGCTCGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 60
 QY 61 GAGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 120
 Db 61 GAGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 120
 QY 121 GGTGCTGAGTGGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 180
 Db 121 GGTGCTGAGTGGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 180
 QY 181 GGGGACGGGCGGAGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 240
 Db 181 GGGGACGGGCGGAGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 240
 QY 241 GGTGCTGCAAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 300
 Db 241 GGTGCTGCAAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 300
 QY 301 GGGGCGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 360
 Db 301 GGGGCGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 360
 QY 361 TACTGCTGACATGCGGCTCATGCGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGG 420
 Db 361 TACTGCTGACATGCGGCTCATGCGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGG 420
 QY 421 CTGGCGGAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCA 480
 Db 421 CTGGCGGAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCA 480
 QY 481 GGTGCTGACAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 540
 Db 481 GGTGCTGACAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 540
 QY 541 GCGGACGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 600
 Db 541 GCGGACGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 600
 QY 601 TACAGCTTGGGCGGAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 660
 Db 601 TACAGCTTGGGCGGAGGAGTGGGGAGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 660

PRIOR APPLICATION NUMBER: 10/274,177
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 10/229,245
PRIOR FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 60/406,296
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 25
LENGTH: 1212
TYPE: DNA
ORGANISM: HUMAN FOXO1
US-10-650-112-25

Query Match 76.3%; Score 923; DB 17; Length 1212;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 180 GGGCGACGGGCAACAGATGCGGAGGCGGCGCGGAGAGCGATCCCGGACG 239
DB 183 GGGCGACGGGCAACAGATGCGGAGGCGGCGCGGAGAGCGATCCCGGACG 242
QY 240 AGCTGTGAGCGGGTGTGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 299
DB 243 AGCTGTGAGCGGGTGTGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 302
QY 300 CGGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 359
DB 303 CGGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 362
QY 360 CTACTGTACATGCGGCTATGCGCATGCGCATGCGCATGCGCATGCGCATG 419
DB 363 CTACTGTACATGCGGCTATGCGCATGCGCATGCGCATGCGCATGCGCATG 422
QY 420 GCTGGGCGGAGATCAAGATGCTCATGCGGCAAGTTCCTTTTCCGCGGACTAC 479
DB 423 GCTGGGCGGAGATCAAGATGCTCATGCGGCAAGTTCCTTTTCCGCGGACTAC 482
QY 480 GGGCTGGCGCACTCCGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539
DB 483 GGGCTGGCGCACTCCGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 542
QY 540 GCGCGACCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599
DB 543 GCGCGACCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 602
QY 600 GTACACCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 659
DB 603 GTACACCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 662
QY 660 GGTCCCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 719
DB 663 GGTCCCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 722
QY 720 CGGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 779
DB 723 CGGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 782
QY 780 CAGCCCCCGGCGGAGGTTCTCAGGCTTCCGCACTTCAGCAGATCTCGGAG 839
DB 783 CAGCCCCCGGCGGAGGTTCTCAGGCTTCCGCACTTCAGCAGATCTCGGAG 842
QY 840 CCGCAGCGGTGCGCTCAGGAGCAAGCGGCGGCGGCGGCGGCGGCGGCGG 899
DB 843 CCGCAGCGGTGCGCTCAGGAGCAAGCGGCGGCGGCGGCGGCGGCGGCGG 902
QY 900 CTGCGCGCGCGCTGCGGCGGCTTCCCGCGGCGGCGGCGGCGGCGGCGG 959
DB 903 CTGCGCGCGCGCTGCGGCGGCTTCCCGCGGCGGCGGCGGCGGCGGCGG 962
QY 960 GCGCGCTGCGGCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1019
DB 963 GCGCGCTGCGGCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1022

QY 1020 GCCACCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1079
DB 1023 GCCACCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1082
QY 1080 ACTCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1139
DB 1083 ACTCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1142
QY 1140 CCTGCAGGCGGCGCT 1153
DB 1143 CCTGCAGGCGGCGCT 1156

RESULT 6

US-10-027-632-231353/c
Sequence 231353, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: Polymorphisms in the Human Genome
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 231353
TYPE: DNA
LENGTH: 585
ORGANISM: Human
US-10-027-632-231353

Query Match 21.8%; Score 264; DB 13; Length 585;
Best Local Similarity 99.5%; Pred. No. 1,9e-115;
Matches 364; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 788 CCGGCAAGTTCTCCAGCTCTTGGCATGACAGATCTTGGCAAGCCCTTCCGAG 847
DB 585 CCGGCAAGTTCTCCAGCTCTTGGCATGACAGATCTTGGCAAGCCCTTCCGAG 526
QY 848 GTGCGCTCAGGAGCAAGCGCGCGGAGAGAGAGCTTCAATGAGGCGCGCGG 907
DB 525 GCGCGCTCAGGAGCAAGCGCGCGGAGAGAGAGCTTCAATGAGGCGCGCGG 466
QY 908 CGTTCGCCCGGCTTCCCGCGGCTTCCCGCGGCGGCGGCGGCGGCGGCGG 967
DB 465 CGTTCGCCCGGCTTCCCGCGGCTTCCCGCGGCGGCGGCGGCGGCGGCGG 406
QY 968 GCGCGTACAGGCGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1027
DB 405 GCGCGTACAGGCGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 346
QY 1028 CCGGCGCGCGCGCTGCTTGAAGCTTCCCGGAGGAGGCGGCGGCGGCGG 1087
DB 345 CCGGCGCGCGCGCTGCTTGAAGCTTCCCGGAGGAGGCGGCGGCGGCGG 286
QY 1088 GCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1147

QY	646	AGCCACCG	653
Db	637	AGCCACCG	644

```

RESULT 10
US-10-650-112-27
; Sequence 27, Application US/10650112
; Publication No. US20040110712A1
; GENERAL INFORMATION:
; APPLICANT: MARKOMITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CWRU-P01-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: RAT FOXQ1
US-10-650-112-27

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Query Match	4.4%	Score 53	DB 17	Length 1203
Best Local Similarity	100.0%	Pred. No.	3.6e-15	
Matches	53	Conservative	0	Mismatches 0; Indels 0; Gaps 0
Qy	601	TACACCTTCGCGAGAGGGCTCTTCGCGCGCGCGCGAAGCGCTTACGCCACCG	653	
Db	592	TACACCTTCGCGAGGGGCTCTTCGCGCGCGCGCGAAGCGCTTACGCCACCG	644	

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RESULT 1
US-10-152-319A-1814
Sequence 1814, Application US/10152319A
Publication No. US20040072160A1
GENERAL INFORMATION:
APPLICANT: Mendick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
PRIORITY FILING DATE: 2002-05-22
PRIORITY APPLICATION NUMBER: US 60/292,335
PRIORITY FILING DATE: 2001-05-22
PRIORITY APPLICATION NUMBER: US 60/297,523
PRIORITY FILING DATE: 2001-06-13
PRIORITY APPLICATION NUMBER: US 60/298,925
PRIORITY FILING DATE: 2001-06-19
PRIORITY APPLICATION NUMBER: US 60/303,810
PRIORITY FILING DATE: 2001-07-10
PRIORITY APPLICATION NUMBER: US 60/303,807
PRIORITY FILING DATE: 2001-07-10
PRIORITY APPLICATION NUMBER: US 60/303,808
PRIORITY FILING DATE: 2001-07-10
PRIORITY APPLICATION NUMBER: US 60/315,047
PRIORITY FILING DATE: 2001-08-28
PRIORITY APPLICATION NUMBER: US 60/324,928
PRIORITY FILING DATE: 2001-09-27
PRIORITY APPLICATION NUMBER: US 60/330,867
PRIORITY FILING DATE: 2001-11-01
PRIORITY APPLICATION NUMBER: US 60/330,462
PRIORITY FILING DATE: 2001-10-22

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; Remaining Prior Application data removed - See File Wrapper or PALM
;
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: patentin Ver. 2.1
; SEQ ID NO 1814
;
; LENGTH: 1760
;
; TYPE: DNA
;
; ORGANISM: Rattus norvegicus
;
; FEATURE:
;
; OTHER INFORMATION: Genbank Accession No. NM_022858
US-10-152-319A-1814

```

Query Match	4.4%	Score 53	DB 12	Length 1760
Best Local Similarity	100.0%	Pred. No. 3	je-15	
Matches 53	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	601	TACACCTTCGCCGAGGCTTCGCGCGCGCGCGCAAGCCCTCAGCCACCG	653	
Db	796	TACACCTTCGCCGAGGCTTCGCGCGCGCGCGCAAGCCCTCAGCCACCG	848	

```

RESULT 12
US-10-029-386-23708
; Sequence 23708, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 3428
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23708
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR2.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
; OTHER INFORMATION: SWISSPROT HIT: Q60688, EVALUATE 1.00e-58
; OTHER INFORMATION: EST HUMAN HIT: AW236501.1, EVALUATE 3.00e-76
; US-10-029-386-23708

```

Query Match	2.5%	Score 30	DB 15	Length 312
Best Local Similarity	100.0%	Pred No. 0.00041		
Matches 30	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	352	AAAGCCCCCTACTGTCATCGCGCCATC	381	
Db	11	AAAGCCCCCTACTGTCATCGCGCCATC	40	

RESULT 13
 US-10-027-632-138699
 ; Sequence 138699, Application US/10027632
 ; Publication No. US2002019837A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12

```

; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 138699
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-138699
```

```

Query Match
2.5%; Score 30; DB 13; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 352 AAGCCCCCTACTCGTACATCGCGCTCATC 381
DB 91 AAGCCCCCTACTCGTACATCGCGCTCATC 120
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```

RESULT 14
US-10-027-632-138700
; Sequence 138700, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 138700
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-138700
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Query Match
2.5%; Score 30; DB 13; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 352 AAGCCCCCTACTCGTACATCGCGCTCATC 381
DB 91 AAGCCCCCTACTCGTACATCGCGCTCATC 120
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```

RESULT 15
US-10-027-632-138701
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```

; Sequence 138701, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 138701
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-138701
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Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 91 AAGCCCCCTACTCGTACATCGCGCTCATC 120
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Search completed: September 2, 2004, 16:44:57
Job time : 612 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 27, 2004, 15:18:23 ; Search time 31.5 Seconds

(without alignments)
3962.908 Million cell updates/sec

Title: US-10-087-080-31

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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Database: Issued Patents AA:

1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
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6: /cgn2_6/prodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	431.5	19.7	553	3	US-09-083-351-2
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3	394.5	18.0	330	4	US-09-083-352-2
4	387	17.7	473	3	US-09-976-594-928
5	347	15.9	480	1	US-08-857-076-99
6	347	15.9	480	1	US-07-882-292-2
7	347	15.9	480	5	US-08-331-644-2
8	336	15.3	347	3	PCT-US93-04102-2
9	333	15.2	106	3	US-08-857-076-100
10	333	15.2	106	3	US-09-083-351-14
11	332	15.2	106	3	US-09-083-352-14
12	332	15.2	106	3	US-09-083-351-15

13	329	15.0	544	4	US-09-087-134-14	Sequence 14, Appl
14	320.5	14.6	106	3	US-09-083-351-12	Sequence 12, Appl
15	320.5	14.6	106	3	US-09-083-352-12	Sequence 12, Appl
16	320.5	14.6	2294	4	US-09-252-991A-1231	Sequence 17231, A
17	319	14.6	365	3	US-09-113-309-2	Sequence 2, Appl1
18	319	14.6	365	3	US-09-521-109-2	Sequence 2, Appl1
19	319	14.6	365	4	US-09-562-332-2	Sequence 2394, A
20	317	14.5	369	4	US-09-252-991A-25394	Sequence 25394, A
21	315	14.4	663	4	US-09-252-991A-10843	Sequence 30843, A
22	314.5	14.4	106	3	US-09-083-351-13	Sequence 13, Appl
23	314.5	14.4	106	3	US-09-083-352-13	Sequence 13, Appl
24	312.5	14.3	783	4	US-09-252-991A-18035	Sequence 18035, A
25	311.5	14.2	686	4	US-09-252-991A-20509	Sequence 20509, A
26	311	14.2	863	4	US-09-252-991A-26099	Sequence 26099, A
27	307	14.0	638	4	US-09-252-991A-27068	Sequence 27068, A
28	307	14.0	957	4	US-09-252-991A-20408	Sequence 20408, A
29	307	14.0	1706	4	US-09-252-991A-31760	Sequence 31760, A
30	305.5	14.0	106	3	US-09-083-351-7	Sequence 7, Appl1
31	305.5	14.0	106	3	US-09-083-352-7	Sequence 7, Appl1
32	304.5	13.9	534	4	US-09-087-134-11	Sequence 11, Appl
33	304.5	13.9	518	3	US-09-252-991A-27110	Sequence 27110, A
34	304.5	13.9	518	3	US-09-113-309-19	Sequence 19, Appl
35	304.5	13.9	518	3	US-09-521-109-19	Sequence 19, Appl
36	304.5	13.9	518	4	US-09-562-332-19	Sequence 18296, A
37	303	13.8	467	4	US-09-252-991A-18296	Sequence 18296, A
38	303	13.8	586	4	US-09-252-991A-24514	Sequence 24514, A
39	303	13.8	720	4	US-09-252-991A-21881	Sequence 21881, A
40	302.5	13.8	726	4	US-09-252-991A-20675	Sequence 20675, A
41	302	13.8	904	4	US-09-976-594-615	Sequence 615, App
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43	297.5	13.2	809	4	US-09-252-991A-31759	Sequence 31759, A
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45	296.5	13.5	495	4	US-09-252-991A-31949	Sequence 31949, A

ALIGNMENTS

RESULT 1
US-09-083-351-2
; Sequence 2, Application US/09083351
; Patent No. 6087107
; GENERAL INFORMATION:
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Stone, Edwin M.
; APPLICANT: Nishimura, Darryl
; APPLICANT: Patel, Shiva
; TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
; TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,351
; FILING DATE: 22-MAY-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UTA-029.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000


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Db      36 GlyGlnAlaThrLeuSerGlyIleTyrArgTyrIleMetGlyArgPheAlaPheTyr 55
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Db      212 SerSerSerCysProAlaPhe---GlyPheProAlaGlyPheSerGlnAlaGluSerPhe 230
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; APPLICANT: Tissenbaum, Heidi
; APPLICANT: Morris, Jason
; APPLICANT: Koweek, Allison
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351001
; CURRENT APPLICATION NUMBER: US/08/857,076C
; CURRENT FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-857-076-99

Alignment Scores:
Pred. No.: 5,77e-16 Length: 473
Score: 387.00 Matches: 124
Percent Similarity: 44.36% Conservative: 45
Best Local Similarity: 32.55% Mismatches: 132
Query Match: 17.68% Indels: 80
Gaps: 15

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298 ProSerGly-----AlaSerAsnProSerAlaAspSerProLeuHisArgGlyValHis 315
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Db 374 SerHisProAlaHisGlyLeu-----AlaProHisGlnSerGlnLeuHisLeu----- 389
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QY 1183 TAC 1185
Db 397 Phe 397

RESULT 5
US-07-882-292-2
; Sequence 2, Application US/07882292
; Patent No. 5324638
; GENERAL INFORMATION:
; APPLICANT: Tao, Wufan
; APPLICANT: Lai, Eseng
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: c/o Cooper and Dunham, 30 Rockefeller
; STREET: Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,292
; FILING DATE: 19920513
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41472
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; TELERX: 422523 COOP UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-07-882-292-2
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Pred. No.: 1,41e-13
Score: 347.00
Percent Similarity: 40.24%
Best Local Similarity: 30.24%
Query Match: 15.85%
DB: 1
Gaps: 17

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QY 178 CAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
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QY 238 GCAGCTGCTCAAGCGGTGTGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 297
Db 147 -----LysLysGlyAlaGlyGlnGlyLys 155
QY 298 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 357
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QY 358 CCTACTGCTACATGCGCTCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 417
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QY 478 ACGGCTGCGCGCACTCCGTGCGCGCAAACTTTGCTTCAAGACTGCTTGTCAAGTGTG 537
Db 214 GlnGlyTrpGlnAsnSerIleArgHisAsnLeuSerLeuAsnLysCysPheValLysVal 233
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Db 234 ProArgHisTrpAspAspPro---GlyLysGlyAsnTrpTrpMetLeuAspProSerSer 252
QY 598 GAGTACACCTTGCAGCGAGGAGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 642
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QY 643 -----CTAGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 690
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QY 691 GCGCGCGCGCG-----CTCGCGCGCGCGCGCG-----CGCGCGCGCG 723
Db 293 ArgAlaGlySerLeuTrpTrpMetSerProPheLeuSerLeuHisIleTrpArgAla 312
QY 724 -----CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 753
Db 313 SerSerThrLeuSerTrpAsnGlyThrThrSerAlaGlyTrpProSerHisProMetProTrp 332
QY 754 TCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 807
Db 333 SerSerValLeuThrGlnAsnSerLeuGlyAsnAsnHisSerPheSerThrAlaAsnGly 352

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QY 907-----CCGCTGC-----CCGGCTTC 921
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QY 922 CCGCGGCTCTCCCGCGGCGGCGCTTCAGAGGCGCTGCTGCGCTGCGCGTACGGCGG 981
Db 412 LProHisProSer-----MetThrSerG 420
QY 982 GCGCAGCCGCGCGGCTGGCGCGCGCGCGAGGCCGAGGTCACCGACCGCGCGCCCTTC 104
Db 420 nhrSerThrSerMetSerAlaArgAlaAlaSerSerThrThrSerProGlnAlaProSe 440
QY 1042 CTGCTTGACCTCTCCCGCGGCGGCGGCC 1069
Db 440 LThrLeuProCysGluSerLeuArgPro 449

RESULT 7
PCT-US93-04102-2
Sequence 2, Application PC/TUS9304102
GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04102
FILING DATE: 19930430
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 41472A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-04102-2

Alignment Scores:
Pred. No.: 1,41e-13 Length: 480
Score: 347.00 Matches: 124
Percent Similarity: 40.24% Conservative: 41
Best Local Similarity: 30.24% Mismatches: 144
Query Match: 15.85% Indels: 101
DB: 5 Gaps: 17

US-10-087-080-31 (1-1209) x PCT-US93-04102-2 (1-480)
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Db 81 ProProGlnAlaArgGlyAlaProAlaAlaAspAspAspGlyGly----- 95

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QY	82	GGGCGGCTCCCGCTG-----TGGGCGGCGGAGAC-----GACTCC	117
Db	96	---ProGlnProLeuLeuLeuLeuProProSerSerAlaLeuAlaAspGlyAlaLysAlaAspAla	114
QY	118	CTGGGCTCAGATGGGACTGCGCGCCAAAGCCGTCCGGCGCGCGCGCAGAGATACG	177
Db	115	LeuGlyAlaLysGlyGlu-----ProGlyGlyGlyProAlaGluLeuAlaPro	130
QY	178	CAGGGCGACGGGGAACAGAGTGGGAGGGCGGGCGGGAGGAGGATCCGGCA	237
Db	131	ValGlyProAspGluLysGluLysGlyAlaGlyAlaGlyGlu-----	146
QY	238	GCAGGTGCTGCACGCGTGTGGCGGAGCGCGGAGCGGGCGCGCGCGCGCGCGG	297
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QY	418	ACGCTGGCGGAGATCAACAGTACTCTATGGGCAAGTTCCCTTTTTCGCGGACACTAC	477
Db	194	ThrLeuAsnGlyIleTyrGluPheIleMetLysAsnPheProTyrThrArgLysAsnLys	213
QY	478	ACGGGCTGGCGCACTCCGTGGCCACCACTTTGGTCAACAGACTGTTTCGCAAGTG	537
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QY	538	CTGCGCGACCCCTCCGCGGCTGGGGGACAGGACAATCTGATGCTCAACCCCAACAGC	597
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QY	598	CAGTACACACTTGCAGCGAGCGGGTCTTCCGCGCGCGCGCAAGCGC-----	642
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QY	808	TTCCGCATGCACAGCATCTCGCGCAG-----CCCTTCGCGACCGCGTCTCAGAGAC	861
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QY	862	ACGGGCGCGCGGAGCAGCGCTCAGTGGGGC---GGCGCGCGCTGCGCGC-----	906
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QY	907	-----CCGCTGC-----CCGCGTTC	921
Db	393	LeuAsnPro-CysSerValAsnLeuLeuAlaGlyGlnThrSerTyrPhePheProHisVa	412
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10 RESULT 10
11 US-09-083-352-14
12 ; Sequence 14, Application US/09083352
13 ; Patent No. 6207450
14 ; GENERAL INFORMATION:
15 ; APPLICANT: Sheffield, Val C.
16 ; APPLICANT: Alward, Wallace L.M.
17 ; APPLICANT: Stone, Edwin M.
18 ; APPLICANT: Nishimura, Darryl
19 ; APPLICANT: Patil, Shiva
20 ; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
21 ; TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
22 ; NUMBER OF SEQUENCES: 22
23 ; CORRESPONDENCE ADDRESS:
24 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
25 ; STREET: One Post Office Square
26 ; CITY: Boston
27 ; STATE: MA
28 ; COUNTRY: USA
29 ; ZIP: 02109-2170
30 ; COMPUTER READABLE FORM:
31 ; MEDIUM TYPE: Floppy disk
32 ; COMPUTER: IBM PC compatible
33 ; OPERATING SYSTEM: PC-DOS/MS-DOS
34 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
35 ; CURRENT APPLICATION DATA:
36 ; APPLICATION NUMBER: US/09/083,352
37 ; FILING DATE: 22-MAY-1998
38 ; CLASSIFICATION: 514
39 ; ATTORNEY/AGENT INFORMATION:
40 ; NAME: Arnold, Beth E.
41 ; REGISTRATION NUMBER: 35,430
42 ; REFERENCE/DOCKET NUMBER: UTA-029.01
43 ; TELECOMMUNICATION INFORMATION:
44 ; TELEPHONE: 617-832-1000
45 ; TELEFAX: 617-832-7000
46 ; INFORMATION FOR SEQ ID NO: 14:
47 ; SEQUENCE CHARACTERISTICS:
48 ; LENGTH: 106 amino acids
49 ; TYPE: amino acid
50 ; STRANDEDNESS:
51 ; TOPOLOGY: linear
52 ; MOLECULE TYPE: protein
53 ; US-09-083-352-14
54 ; Alignment Scores:
55 ; Pred. No.: 9.13e-13
56 ; Length: 106

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RESULT 11
 US-09-083-351-15
 ; Sequence 15, Application US/09083351
 ; Patent No. 6087107
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheffield, Val C.
 ; APPLICANT: Alward, Wallace L.M.
 ; APPLICANT: Stone, Edwin M.
 ; APPLICANT: Nishimura, Darryl
 ; APPLICANT: Patel, Shiva
 ; TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
 ; TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
 ; TITLE OF INVENTION: TRANSCRIPTION FACTOR
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109-2170
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/083,351
 ; FILING DATE: 22-MAY-1998
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Arnold, Beth E.
 ; REGISTRATION NUMBER: 35,430
 ; REFERENCE/DOCKET NUMBER: UIA-029.02
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 106 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-083-351-15

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: other
 LOCATION: 1...1
 OTHER INFORMATION: Human FAST-1
 US-09-087-134-14

Alignment Scores:
 Score: 1.68e-12 Length: 544
 329.00 Matches: 111
 Percent Similarity: 37.57% Conservative: 31
 Best Local Similarity: 29.37% Mismatches: 130
 Query Match: 15.03% Indels: 107
 DB: 4 Gaps: 13

US-10-087-080-31 (1-1209) x US-09-087-134-14 (1-544)

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 QY 385 ATGCGCATCGCGAGCTCGCGCGCGCGCGCTTACGCTGCGCGAGATCAACGATACCTC 444
 DB 44 LeuValIleGlnIleAlaIleProSerArgArgLysLeuAlaGlnIleIleArgGlnVal 63
 QY 445 ATGCGCAAGTCCCTTTTCCGCGGAGCTACAGCGAGCTCGCGCAATCCGCGCGCAC 504
 DB 64 GlnAlaValPheProPhePheArgLysArgLysArgLysArgLysArgLysArgLys 83
 QY 505 AACCTTTCGCTCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
 DB 84 AsnLeuSerSerAsnArgCysPheArgLysValProLysAspProAlaLysProGlnAla 103
 QY 565 AAGGACACTACTGATGCTC 585
 DB 104 LysGlyAsnIlePheIleValAlaValSerLeuIleProAlaGlnIleAlaValArgLeuGln 123
 QY 586 -----AACCCCAACGAGGAGTACACCTTCCGCGAGGAG 618
 DB 124 AsnThrAlaLeuCysArgArgTrpGlnAsnGlyGlyAlaArgGlyAlaPheAla--LysA 143
 QY 619 GTCTTCCGCG-----CCGCGCGAAGCGCTCAGCCAC 651
 DB 143 sPLeuGlyProIleValLeuHisGlyArgProTrpArgProProSerProProProP 163
 QY 652 CGCGCGCGGT-----CCCGCG 669
 DB 163 roSerGlnIlePheSerIleLysSerLeuLeuArgArgSerGlyGlnIleAlaPro--Trp 182
 QY 670 CCCGAGCTCGCGCGCGAGGAGGCGCG----- 696
 DB 183 ProGlnIleAlaIleProGlnAsnSerProValProAlaGlyThrGlyAsnAsnGlyGln 202
 QY 697 GGCCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 756
 DB 203 AlaValProIleProProIleProSerSerGlnArgProLeu--TrpProLeuCyserole 222
 QY 757 CCGG---CCGCGCGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 813
 DB 222 uProGlyProIleArgValGlnGlyGlyThrValGlnGlyAlaMetGlyProGlnIle 242
 QY 814 ATGCACAGCATCTCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 873
 DB 242 oSerProGlnIle---LeuGlyProGlyLeuSerThrThrAlaGlnHisArgSerSerI 261
 QY 874 AGCAGGCTT-----CAGTGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 911
 DB 261 yGlyArgSerSerGlyGlyHisArgAlaSerLeuTrpGlnIleLeuProThrSerTy 281
 QY 912 GCGCGGTTGCGCG-----GCGCTCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCT 965
 DB 912 GCGCGGTTGCGCG-----GCGCTCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCT 965

DB 281 uProIleTyThrProAsnValAlaMetProLeuAlaProProProThrSerCysProG 301
 QY 966 CTGCGGCTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1025
 DB 301 nCysPro-----SerThrSerProAlaIleTyTrpGlyVal-----AlaProG 315
 QY 1026 GACG---GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
 DB 315 uThrArgGlyProProGlyLeuLeuCysAspLeuAlaLeuPheGlnGlyValProPr 335
 QY 1081 -----CTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1097
 DB 335 oAsnLysSerIleTyArgValTrpValSerHisProArgAspLeuAlaIleProGlyPr 355
 QY 1098 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1119
 DB 355 oGlyTrpLeuLeuSerTrpCysSerLeu**GlySer**AspArgGlyArgSerSerIle 375

RESULT 14
 US-09-083-351-12
 Sequence 12, Application US/09083351
 Patent No. 6087107

DB 375 uProLeuProProProProCys**GlnGlyAlaLysAlaArgArg 390

GENERAL INFORMATION:
 APPLICANT: Sheffield, Val C.
 APPLICANT: Alward, Wallace L.M.
 APPLICANT: Stone, Edwin M.
 APPLICANT: Nishimura, Daryll
 APPLICANT: Patil, Shiva

TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
 TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/083,351
 FILING DATE: 22-MAY-1998

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Arnold, Beth E.
 REGISTRATION NUMBER: 35,430
 REFERENCE/DOCKET NUMBER: UTA-029.02
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 106 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-083-351-12

Alignment Scores:
 Pred. No.: 5.09e-12 Length: 106
 Score: 320.50 Matches: 61
 Percent Similarity: 71.43% Conservative: 14
 Best Local Similarity: 58.10% Mismatches: 29

Query Match: 14.64% Indels: 1
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 Db 22 SerProIYsIysArgLeuThrLeuSerGluIleCysGluPheIleSerGlyArgPhePro 41
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 QY 460 TTTTTCGGGGGAGCTACACAGGGCTGGCGCACTCCGTCGCGCAACAACCTTGCTCAAC 519
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 Db 42 TyrTyrArgGluIYsPheProAlaTrpGlnAsnSerIleArgHisAsnLeuSerLeuAsn 61
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 QY 580 ATGCTCAACCCCAACAGCGAGTACACCTTGCGCGAGGGGTCTTCGCGCGCGCGCGAC 639
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 Db 81 ThrLeuAspProGluSerAlaAspMetPheAspAsnGlySerPheLeuArgArgGly 100
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 Db 101 ArgPheIYsArgGln 105
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 RESULT 15
 US-09-083-352-12
 ; Sequence 12, Application US/09083352
 ; Patent No. 6207450
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheffield, Val C.
 ; APPLICANT: Alward, Wallace L.M.
 ; APPLICANT: Stone, Edwin M.
 ; APPLICANT: Nishimura, Darryl
 ; APPLICANT: Patel, Shiva
 ; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
 ; TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: POLEY, HOAG & ELLIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109-2170
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/083.352
 ; FILING DATE: 22-MAY-1998
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Arnold, Beth E.
 ; REGISTRATION NUMBER: 35,430
 ; REFERENCE/DOCKET NUMBER: UIA-029.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 106 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-083-352-12

Alignment Scores:
 Pred. No.: 5,09e-12 Length: 106
 Score: 320.50 Matches: 61
 Percent Similarity: 71.43% Conservative: 14
 Best Local Similarity: 58.10% Mismatches: 29
 Query Match: 14.64% Indels: 1
 DB: 3 Gaps: 1
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 |||||
 Db 2 ThrArgLeuValIysProProIYrSerTyrIleAlaLeuIleThrMetAlaIleLeuGln 21
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 QY 400 TCGCGGGGGGGGGCTTGACCTGCGGGAGATCAACGAGTACCTCATGGGCAAGTTCCCC 459
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 Db 22 SerProIYsIysArgLeuThrLeuSerGluIleCysGluPheIleSerGlyArgPhePro 41
 |||||
 QY 460 TTTTTCGGGGGAGCTACACAGGGCTGGCGCACTCCGTCGCGCAACAACCTTGCTCAAC 519
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 Db 42 TyrTyrArgGluIYsPheProAlaTrpGlnAsnSerIleArgHisAsnLeuSerLeuAsn 61
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 QY 520 GACTGCTTGCTCAAGGTCTGCGCGACCCCTCGCGGCTTGCGGGCAAGCAACTACTGG 579
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GenCore version 5.1.6
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Maximum Match 100%

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Published Applications AA:
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	2123	97.0	402	16	US-10-650-112-18
5	2081.5	95.1	403	16	US-10-650-112-22
6	1597	73.0	400	16	US-10-650-112-23
7	1534	70.1	400	16	US-10-650-112-24
8	517	23.6	465	14	US-10-205-823-136
9	429.5	19.6	553	10	US-09-292-862-2
10	415.5	19.0	376	14	US-10-007-280A-221
11	388.5	17.7	19662	15	US-10-084-846A-6
12	387	17.7	473	9	US-09-844-353A-99
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25	338.5	15.5	19725	15	US-10-084-846A-4
26	338	15.4	509	16	US-10-471-450-11
27	336	15.3	347	9	US-09-844-353A-100
28	336	15.0	19608	15	US-10-084-846A-8
29	329	15.0	544	13	US-10-044-442-14
30	325.5	14.9	625	16	US-10-437-963-165015
31	323.5	14.4	19723	15	US-10-084-846A-5
32	322	14.7	497	16	US-10-437-963-125004
33	315.5	14.0	19695	15	US-10-084-846A-3
34	311.5	14.2	514	16	US-10-437-963-111701
35	306.5	14.0	417	9	US-09-963-285-4
36	305.5	14.0	534	13	US-10-044-442-11
37	305	13.9	503	12	US-10-425-114-64093
38	304.5	13.6	19725	15	US-10-084-846A-4
39	303.5	13.9	437	16	US-10-437-963-168762
40	302.5	13.8	797	14	US-10-156-761-10907
41	301.5	13.4	595	9	US-09-738-973-187
42	301.5	13.4	595	9	US-09-854-133-187
43	301.5	13.4	595	14	US-10-144-659A-281
44	297.5	13.6	2263	16	US-10-408-765A-1231
45	294	13.4	316	12	US-10-425-114-57324

ALIGNMENTS

RESULT 1
US-10-229-345-18
; Sequence 18, Application US/10229345
; Publication No. US20040038220A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; FILE REFERENCE: CWRU-P01-003
; CURRENT APPLICATION NUMBER: US/10/229,345
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-229-345-18

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:
7.07e-93	2123.00	100.00%	100.00%	96.98%

Length:	Matches:	Conservative:	Mismatches:	Indels:
402	402	0	0	0

DB: 12 Gaps: 0

US-10-087-080-31 (1-1209) x US-10-229-345-18 (1-402)

QY 1 ATGAAGTTGAGGAGTGTTCCTCGCGCGGCCCAAGGAGCAAGAGGCACTGACTG 60

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QY 61 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

Db 21 GluGlyAlaGlySerAspAlaProSerProLeuSerAlaIahGlyAspSerLeu 40

QY 121 GGCTCAGATGGGAGCTCGCGCGCAAGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Db 41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyAlaAlaGAspThrGln 60

QY 181 GGGGACGGCGCAAGACTGCGGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240

Db 61 GlyAspGlyGlnGlnSerAlaGlyGlyProGlyAlaGlnAlaIahLeuProAlaAla 80

QY 241 GGTGCTGCAAGCGGTGCGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

Db 81 AlaAlaAlaAlaValAlaAlaGlnGlyAlaGlnAlaGlyAlaAlaGlyProGlyAlaGly 100

QY 301 GCGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360

Db 101 GlyAlaGlySerGlyGlnGlyAlaArgSerLysProGlyThrArgArgProLysProPro 120

QY 361 TACTGTACATCGGCTCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 420

Db 121 TySerTyrIleAlaLeuIleAlaMetAlaIleArgSerAlaGlyAlaArgLeuThr 140

QY 421 CTGGCGGAGATCAACGAGTACCTCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

Db 141 LeuAlaGlnIleAsnGlnTyrLeuMetGlyLysPheProPheArgGlySerTyrThr 160

QY 481 GGGTGGCGCACTCGTGGCGCAACACTTTCGCTCAACGACTGCTTCGTCAGAGTGTG 540

Db 161 GlyTyrPargAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeu 180

QY 541 CGCGACCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

Db 181 ArgAspProSerArgProTyrGlyLysAspAsnTyrTyrMetLeuAsnProAsnSerGln 200

QY 601 TAGACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660

Db 201 TyrThrPheAlaAspGlyValPheArgArgArgLysArgLysSerHisAlaGlyAlaPro 220

QY 661 GTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720

Db 221 ValProAlaProGlyLeuArgProGlnGlnAlaProGlyLeuProAlaAlaProProPro 240

QY 721 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780

Db 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGlnAlaArgAla 260

QY 781 AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840

Db 261 SerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuAlaGlyLysProPhe 280

QY 841 CGCAGCGCTGCGCTCAGGAGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900

Db 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTyrGlyAlaAlaPro 300

QY 901 TGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960

Db 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320

QY 961 CGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020

Db 321 ProLeuCysAlaTyrGlyAlaGlyLysProAlaArgLysGlyAlaArgLysGlnAlaGlyVal 340

QY 1021 CCAACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080

Db 341 ProProThrAlaProProLeuLeuAlaProLeuProAlaAlaAlaProAlaLysPro 360

QY 1081 CTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140

Db 361 LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380

QY 1141 CTGACGAGCGCGCTTACGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200

Db 381 LeuGlnAlaAlaLeuValAlaArgArgProGlyProHisLeuSerTyrProValGlnThrLeu 400

QY 1201 CTAGCT 1206

Db 401 LeuAla 402

RESULT 2

US-10-274-177-18

/ Sequence ID, Application US/10274177

/ Publication No. US20040038225A1

/ GENERAL INFORMATION:

/ APPLICANT: MARKWITZ, Sanford D.

/ TITLE OR INVENTION: METHODS FOR CATEGORIZING PATIENTS

/ FILE REFERENCE: CWRU-P01-003

/ CURRENT APPLICATION NUMBER: US/10/274,177

/ PRIOR FILING DATE: 2002-10-18

/ PRIOR APPLICATION NUMBER: US/10/229,345

/ PRIOR FILING DATE: 2002-08-26

/ NUMBER OF SEQ ID NOS: 20

/ SOFTWARE: Patent version 3.1

/ SEQ ID NO 18

/ LENGTH: 402

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-274-177-18

Alignment Scores:

Pred. No.: 7.07e-93 Length: 402

Score: 2123.00 Matches: 402

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 96.98% Indels: 0

DB: 12 Gaps: 0

US-10-087-080-31 (1-1209) x US-10-274-177-18 (1-402)

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Db 1 MetLysLeuGluValPheValProAlaGAlaIahIseGlyAspLysGlnGlySerAspLeu 20

QY 61 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

Db 21 GluGlyAlaGlySerAspAlaProSerProLeuSerAlaIahGlyAspSerLeu 40

QY 121 GGCTCAGATGGGAGCTCGCGCGCAAGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Db 41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyAlaAlaArgAspThrGln 60

QY 181 GGGGACGGCGCAAGACTGCGGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240

Db 61 GlyAspGlyGlnGlnSerAlaGlyGlyProGlyAlaGlnAlaIahLeuProAlaAla 80

QY 241 GGTGCTGCAAGCGGTGCGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

Db 81 AlaAlaAlaAlaValAlaAlaGlnGlyAlaGlnAlaGlyAlaAlaGlyProGlyAlaGly 100

QY 301 GCGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360

Db 101 GlyAlaGlySerGlyGlnGlyAlaArgSerLysProGlyThrArgArgProLysProPro 120

QY 361 TACTGTACATCGGCTCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 420

Db 121 TySerTyrIleAlaLeuIleAlaMetAlaIleArgSerAlaGlyAlaArgLeuThr 140

QY 421 CTGGCGGAGATCAACGATCACTCATGGGCAAGTCCCTTTTCCGGCGGACCTACAG 480
 Db 141 LeuAlaIuIleasnGluYrIleuMeGlyLysPheProPhePheArgGlySerYrThr 160
 QY 481 GGCTGGGCAACTCCGCGCCCAACACTTTCGTCAAGACAGCTTCCGCAAGGCTG 540
 Db 161 GYrTyrPargnservValArgHisasnLeuSerLeuasnSpysPheValIysValLeu 180
 QY 541 CGGACCCCTCGCGGCGCTGGGGCAAGCAACTACTGATGCTCAACCCCAACAGGAG 600
 Db 181 ArgAspProserArgProTyrGlyLysAspAsnYrTrpMetLeuasnProAsnserGlu 200
 QY 601 TACACCTTGGCCGACGAGGCTTTCGCGCGCGCAAGGCTTCAAGCCACGCGCGCG 660
 Db 201 TyrThrPheAlaaspGlyValPheArgArgArgArgLysArgLeuSerHisArgAlaPro 220
 QY 661 GTCCCGCGCGCGCGCTGGCGCGGAGAGAGAGCGCGCGCTCCCGCGCGCGCGCGCG 720
 Db 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
 QY 721 GCGCGCGCGCGCGCGCGCTGCGCGCGCATGCGCTCGCGCGCGCGCGCGCGCGCGCG 780
 Db 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGlnGluArgAla 260
 QY 781 AGCCCGCGCGCGCAAGTTCCTCAGCTCTTTCGCGCATGACAGCATCTCGCGCAAGCCCTT 840
 Db 261 SerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPhe 280
 QY 841 CGGAGCGCTGCGCTCAGGGAACAAGCGCGCGCGCGCAAGCTTCAAGTGGGCGCGCGCG 900
 Db 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrpGlyAlaAlaPro 300
 QY 901 TGCCTGCGCGCGCGCGCTTCCCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCG 960
 Db 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
 QY 961 CGGCTTGGCGGTAACGCGCGCGCGCGCGCGCGCGCGCTGGCGCGCGCGCGCGCGAG 1020
 Db 321 ProLeuCysAlaIleTyrlGlyAlaGlyLeuProAlaArgLeuGlyAlaArgGlnAlaGlnVal 340
 QY 1021 CCACGCAACGCGCGCGCGCTTTCGCTTGAACCTGCTCCCGCGCGCGCGCGCGCGCGCA 1080
 Db 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaIysPro 360
 QY 1081 CTCGCAAGCGCGCGCGCGCGCGCGCGCACTGTACTGCGCGCGCGCGCGCGCGCGCG 1140
 Db 361 LeuArgGlyProAlaAlaGlyGlyAlaHisLeuYrCysProLeuArgLeuProAlaAla 380
 QY 1141 CTCGAGGCGCGCTTACTCGGNGCTCTGGCGCGCGCACTGTCTGTAACCGGTAAGAGC 1200
 Db 381 LeuGlnAlaAlaLeuValArgArgProGlyProHisLeuSerYrProValGlnThrLeu 400
 QY 1201 CTAGCT 1206
 Db 401 LeuAla 402
 RESULT 3
 US-10-087-080-32
 ; Sequence 32, Application US/10087080
 ; Publication No. US20030235820A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Markowitz, Sanford David
 ; APPLICANT: Eos Biotechnology, Inc.
 ; APPLICANT: Case Western Reserve University
 ; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal
 ; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
 ; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
 ; FILE REFERENCE: 018501-000840US
 ; CURRENT APPLICATION NUMBER: US/10/087,080
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: US 60/272,206
 ; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: US 60/281,149
 ; PRIOR FILING DATE: 2001-04-02
 ; PRIOR APPLICATION NUMBER: US 60/284,555
 ; PRIOR FILING DATE: 2001-04-17
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 402
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: winged helix/forkhead transcription factor (HNF1)
 ; US-10-087-080-32
 Alignment Scores:
 Pred. No.: 7.07e-93 Length: 402
 Score: 2123.00 Matches: 402
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.98% Indels: 0
 DB: 15 Gaps: 0
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 Db 1 MetLysLeuGlnValPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20
 QY 61 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 Db 21 GlnGlyAlaGlyGlySerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
 QY 121 GGCTCAGATGGAGGACTCGCGCGCGCGCGCAAGCCGTCGCGCGCGCGCGCGCGCGCG 180
 Db 41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyAlaArgAspThrGln 60
 QY 181 GCGCAGCGGGAACAAGATCGGGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 240
 Db 61 GlyAspGlyGlnGlnSerAlaGlyGlyGlyProGlyAlaGlnGlnAlaLeuProAlaAla 80
 QY 241 GCTGCTGCAACGCGTGGTGGCGGAGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCG 300
 Db 81 AlaAlaAlaAlaValAlaValAlaGlnGlyAlaGlnAlaGlyAlaAlaGlyProGlyAlaGly 100
 QY 301 GCGCGCGGAGAGGCGGAGGCGTGCACGACGACGATATACGCGCGCGCGCGCGCGCGCG 360
 Db 101 GlyAlaGlySerGlyGlnGlyAlaArgSerLysProYrThrArgArgProLysProPro 120
 QY 361 TACTGTCATATCGCTCATCGCATGCGCATCGCGACTCGCGCGCGCGCGCGCGCGCTGACG 420
 Db 121 TyrSerYrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThr 140
 QY 421 CTGGCGGAGATCAACGACTCACTCATGGGCAAGTTCCTTTTCCGGCGGACTACAGC 480
 Db 141 LeuAlaGlnIleAsnGluYrIleuMetGlyLysPheProPhePheArgGlySerYrThr 160
 QY 481 GGTGGCGCAACTCCGCGCCCAACACTTTCGTCAAGACAGCTTCCGCAAGGCTG 540
 Db 161 GYrTyrPargnservValArgHisasnLeuSerLeuasnSpysPheValIysValLeu 180
 QY 541 CGGACCCCTCGCGGCGCTGGGGCAAGCAACTACTGATGCTCAACCCCAACAGGAG 600
 Db 181 ArgAspProserArgProTyrGlyLysAspAsnYrTrpMetLeuasnProAsnserGlu 200
 QY 601 TACACCTTGGCCGACGAGGCTTTCGCGCGCGCAAGGCTTCAAGCCACGCGCGCGCG 660
 Db 201 TyrThrPheAlaaspGlyValPheArgArgArgArgLysArgLeuSerHisArgAlaPro 220
 QY 661 GTCCCGCGCGCGCGCTGGCGCGGAGAGAGAGCGCGCGCTCCCGCGCGCGCGCGCGCG 720
 Db 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
 QY 721 GCGCGCGCGCGCGCGCGCTGCGCGCGCATGCGCTCGCGCGCGCGCGCGCGCGCGCGCG 780

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Db      241  |||||
AlaProAlaAlaProAlaSerProAlaArgSerProAlaArgInguAlaAla 260
QY      781  AGCCCCGCGGCAAGTTCTCCAGCTCTTGGCCATGCAGACATCTGCGCAAGCCCTTC 840
Db      261  SerProAlaGlyPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPhe 280
QY      841  CGAAGCGTGTGCTCAGAGGACACAGCGCCCGGAGCGACGCTTCAAGTGGGCGCGCGCC 900
Db      281  ArgSerArgArgLeuAlaAspThrAlaProGlyThrThrLeuGlnTrpGlyAlaAlaPro 300
QY      901  TGCCCGCGCTGCGCGCGCTCCCGCGCTCTCCCGCGCGCGCTGCAAGAGCCCTGCTG 960
Db      301  CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
QY      961  CCGCTCTGCGCGTACGGCGCGGCGAGCGCGCGCTGCGCGCGCGCGCGCGAGGTG 1020
Db      321  ProLeuCysAlaTyrglyAlaGlyGlnProAlaArgLeuGlyAlaArgGlnAlaGlnVal 340
QY      1021  CCAACCGACCGCGCGCGCCCTCTGCTTGCACCTCTCCCGCGCGCGCGCGCGCAAGCCA 1080
Db      341  ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysPro 360
QY      1081  CTCGAGAGCGCGCGCGCGCGCGCGACACCTGTACTGCCCTGCGCGCTGCGCGCAGCC 1140
Db      361  LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrcysProLeuArgLeuProAlaAla 380
QY      1141  CTGCGAGCGCGCTTATGTCGAGCGTCTGCGCGCGACCTGTGCTGACCGCGGTGAGAGCCTC 1200
Db      381  LeuGlnAlaAlaLeuValAlaArgArgProGlyProHisLeuSerTyrcysProAlaGlnThrLeu 400
QY      1201  CTAGCT 1206
Db      401  LeuAla 402

RESULT 4
US-10-650-112-18
; Sequence 18, Application US/10650112
; Publication No. US20040110712A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CWRU-P01-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 402
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-650-112-18

Alignment Scores:
Pred. No.: 7.07e-93 Length: 402
Score: 2123.00 Matches: 402
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.98% Indels: 0
Gaps: 0
DB: 16

US-10-087-080-31 (1-1209) x US-10-650-112-18 (1-402)
QY      1  ATGAAGTTGAGGAGTGTCTCCCTCGCGCGCGCAAGCGGAGCAAGACAGGAGAGTACCTG 60
Db      1  MetLysLeuGlnValPheValProAlaArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20

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QY      61  GAGGCGCGGCGGCGGCGGCGAGCGAGCCGCTCCGCTGTGCGCGCGGAGAGCACTCCCTG 120
Db      21  GlnGlyAlaGlycylSerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
QY      121  GGCTCAGATGGGAGATGCGCGGCGCAAGCCGTCGCGGCGCGGCGCGCGCAGAGATACGAG 180
Db      41  GlySerAspGlyAspCysAlaAlaLysProSerAlaGlycylGlyAlaAlaGAspThrGln 60
QY      181  GCGGAGCGGAGAAAGAGTGTGCGGAGCGGCGGCGGAGCGCGGCGGCGGCGCGCGCGAGCA 240
Db      61  GlyAspGlyGlnGlnSerAlaGlyGlyGlyProGlyAlaGlnGlnAlaIleProAlaAla 80
QY      241  GCTGCTGCAAGCGGTGTGCGGAGGCGCGGAGCGCGGCGGCGGCGGCGCGCGCGCGCG 300
Db      81  AlaAlaAlaAlaValValAlaGlnGlnGlyAlaGlnAlaGlyAlaAlaGlyProGlyAlaGly 100
QY      301  GCGCGCGGAGCGCGCGCGGAGGCTGACGACGAGAACCATATACGCGGCGGCGCGCGCGCG 360
Db      101  GlyAlaGlySerGlyGlnGlyAlaArgSerLysProTyrcysArgArgProLysProPro 120
QY      361  TACTGTACATGCGGCTCATGCGCATGCGCATGCGGACTCGGCGGCGGCGGCGGCTTGACG 420
Db      121  TyrcysThrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThr 140
QY      421  CTGCGGAGATCAACAGTACTCATGCGCAGTCCCTTTTCCGCGGCGAGCTACAG 480
Db      141  LeuAlaGlnIleAsnGlnIleuMetGlyLysPheProPheArgGlySerTyrcysThr 160
QY      481  GGCTGGCGCAACTCCGTCGCGCGCAACCTTCCGCTCAACAGACTGCTTCGTCMAAGTCTG 540
Db      161  GlyTrpArgAsnSerValArgGlnAsnLeuSerLeuAsnAspCysPheValLysValLeu 180
QY      541  CGGAGCCCTCGCGGCGCTGCGGCGGAGAGCAACTAGATGATGATCAACCCCAACAGCAG 600
Db      181  ArgAspProSerArgProTrpGlyLysAspAsnTyrcysMetLeuAsnProAsnSerGln 200
QY      601  TACACCTTGCAGCAGCGGAGTCTTCCGCGCGCGCGGCGAGCGCTTACGCCACCGCGCGCG 660
Db      201  TyrThrPheAlaAspGlyValPheArgArgArgLysArgLeuSerHisArgAlaPro 220
QY      661  GTCCCGCGCGCGCGCGCTGCGGCGGAGAGGCGCGCGCGCTCCCGCGCGCGCGCGCGCG 720
Db      221  ValProAlaProGlyLeuAspProGlnGlnAlaProGlyLeuProAlaAlaProProPro 240
QY      721  GCGCGCGCGCGCGCGCTGCGCGCGCATGCGCTGCGCGCGCGCGCGCAGAGAGCGCGCG 780
Db      241  AlaProAlaAlaProAlaSerProArgMetArgSerProAlaAlaGlnGlnGlnAlaAla 260
QY      781  AGCCCCGCGGCAAGTTCTCCAGCTCTTGGCCATGCAGACATCTGCGCAGCCCTTC 840
Db      261  SerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPhe 280
QY      841  CGAAGCGTGTGCTCAGAGGACACAGCGCCCGGAGCGAGCGCTTCAAGTGGGCGCGCGCC 900
Db      281  ArgSerArgArgLeuAlaAspThrAlaProGlyThrThrLeuGlnTrpGlyAlaAlaPro 300
QY      901  TGCCCGCGCTGCGCGCGCTCCCGCGCTCTCCCGCGCGCGCTGCAAGAGCCCTGCTG 960
Db      301  CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
QY      961  CCGCTCTGCGCGTACGGCGCGGCGAGCGCGCGCTGCGCGCGCGCGCGCGAGGTG 1020
Db      321  ProLeuCysAlaTyrglyAlaGlyGlnProAlaArgLeuGlyAlaArgGlnAlaGlnVal 340
QY      1021  CCAACCGACCGCGCGCGCCCTCTGCTTGCACCTCTCCCGCGCGCGCGCGCGCAAGCCA 1080
Db      341  ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysPro 360
QY      1081  CTCGAGAGCGCGCGCGCGCGCGCGACACCTGTACTGCCCTGCGCGCTGCGCGCAGCC 1140
Db      361  LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrcysProLeuArgLeuProAlaAla 380
QY      1141  CTGCGAGCGCGCTTATGTCGAGCGTCTGCGCGCGACCTGTGCTGACCGCGGTGAGAGCCTC 1200

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: ORGANISM: MOUSE FOXQ1
US-10-650-112-23

Alignment Scores:
Pred. No.: 5.04e-68 Length: 400
Score: 1597.00 Matches: 320
Percent Similarity: 82.27% Conservative: 14
Best Local Similarity: 78.82% Mismatches: 62
Query Match: 72.96% Indels: 10
DB: 16 Gaps: 6

US-10-087-080-31 (1-1209) x US-10-650-112-23 (1-400)

QY 1 ATGAAGTTGAGGAGTTCCTGCTCCGCGGCGCCAGGAGGAGCAAGAGGAGGAGTGAAGCTG 60
Db 1 MetLysLeuGluValPheValProArgAlaIahISglYasPluMserGlySerAspLeu 20
QY 61 GAGGCGCGGCGGCGGAGCGAGCGCGCTGCCGCTGTGCGGCGGAGAGAGTCCCTG 120
Db 21 GluGlyAlaGlySerSerAspValProSerProLeuSerAlaIahISglYasPluSerLeu 40
QY 121 GGCTCAATGGGAGCTGCGCGGCC---AAGCGTCCGCGGCGGCGGCGGCGGAGATACG 177
Db 41 GlySerAspGlyAspCysAlaIahISglYasPluSerProAlaIahISglYasPluSerLeu 60
QY 178 CAG---GGCGAGCGGCGGAGGAGGAGGAGGCGGCGGCGGCGGCGGCGGAGGATCCG 234
Db 61 GluGlyAlaGlyGlyGlyGluArgAsnSerSerGlyGlyProSerAlaIahISglYasPlu 80
QY 235 GCAGACAGCTGCTGCAGCGGCTGTGTGCGGAGGCGCGGAGGCGGCGGCGGCGGCGGCG 294
Db 81 AlaThrAspAspSerArg-----ThrGlnAlaSerAlaIahISglYasPluSerCys 95
QY 295 GCGGCGGCGGCGGCGGAGCGGCGGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGG 354
Db 96 AlaGlyAlaGlyAlaGlyGlyGlyGluGlyAlaIahISglYasPluSerProIleArgArgProLys 115
QY 355 CCCCCCTACTGTCATCGGCTCATGCGCCGTCATGCGGAGGAGGAGGAGGAGGAGGAGG 414
Db 116 ProProIleSerIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 135
QY 415 TTGACGCTGGCGGAGATCAACAGACTCATGTGCGCAAGTTCCCTTTTTCGCGGCGAGC 474
Db 136 LeuThrLeuAlaGluIleAsnGluIleuMetGlyLysPheProPheArgGlySer 155
QY 475 TACACGGGCTGCGGCACTCCGTGCGGCAACACTTTCGCTCAACGACTGTTGTCAAG 534
Db 156 TyrThrGlyTyrPArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLys 175
QY 535 GTGCTGGCGGCGAGCCCTGCGGCGCTGGGCGCAAGCACTGAGATGCTCAACCCCAAC 594
Db 176 ValLeuArgAspProSerArgProIleIleIleIleIleIleIleIleIleIleIleIle 195
QY 595 AGCAGATACACTTTCGCGGAGGAGTCTTCGCGCGGCGGCGGCAAGCGGCTCAGCACCGC 654
Db 196 SerGluTyrThrPheAlaAspGlyValPheArgArgGlyArgLeuSerHisArg 215
QY 655 GCGCGGCTCCCGCGGCGGCTGCGGCGGAGAGGAGGCGGCGGCTCCCGGCC---GCC 711
Db 216 ThrThrValSerAlaSerGlyLeuArgProGlnGluAlaProProGlyProAlaGlyThr 235
QY 712 CCGCGCGCGCGCGCGCGCGCGCGCTGCGGCGGAGTCCGCTGCGGCGGCGGCGGAGAG 771
Db 236 ProGlnProAlaProAlaIahISglYasPluSerProIleIahISglYasPluSerProAlaArgGln 255
QY 772 GAGGCGCGGAGCGCGCGGCGGAGGTTCTCAAGTCTCTTCGCGCATGAGCAGCATCTCGGC 831
Db 256 GluArgSerSerProAlaSerLysPheSerSerSerPheAlaIleAspSerLysLeuSer 275
QY 832 AAGCCCTTCGCGGAGCGCTGCTCAAGGAGCAAGCGGCGGCGGAGAGGAGGAGGAGGAGG 891
Db 276 LysProPheArgSerArgArgAspGlyAspSerAlaLeuGlyValGlnLeuProIleProIle 295

```

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QY 892 GCCGCGGCTTCGCGGCGGCTGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGG 951
Db 296 AlaIahProCysProProLeuAlaGlyAlaTyrProAlaLeuLeuProAlaIahISglY 315
QY 952 GCCCTGCTGCGGCTTCGCGGCTACGCGGCGGCGGAGCGGCGGCGGCGGCGGCGGAG 1011
Db 316 AlaLeuLeuProLeuCysAlaTyrGlyAlaSerGluProThrLeuAlaIahISglY 335
QY 1012 GCCGAGGTGCACGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1071
Db 336 ThrGluValGlnProAlaAla---ProLeuLeuLeuAlaProLeuSerThrAlaAlaPro 354
QY 1072 GCCAAGCCTCTCGAGGCGCG---GCCGCGGCGGCGGCGGCGGAGTGTACTGCGGCGG 1128
Db 355 AlaLysProPheArgGlyProGlnThrAlaGlyAlaIahISglYasPluSerProLeuArg 374
QY 1129 CTGCGCGGAGCGCTGCGAGGCGGCGCTTATGTCGAGCTGCTGCGGCGGAGCTGTGATCCG 1188
Db 375 LeuProThrAlaLeuGlnAlaIahISglYasPluSerProIleIleIleIleIleIleIle 394
QY 1189 GTGGAGACGCTCTAGCT 1206
Db 395 ValGlnThrLeuLeuAla 400

RESULT 7
US-10-650-112-24
: Sequence 24, Application US/10650112
: Publication No. US20040110712A1
: GENERAL INFORMATION:
: APPLICANT: MARROWITZ, Sanford D.
: TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
: FILE REFERENCE: CWRU-P01-044
: CURRENT APPLICATION NUMBER: US/10/650,112
: PRIOR FILING DATE: 2003-08-26
: PRIOR APPLICATION NUMBER: 10/274,177
: PRIOR FILING DATE: 2002-10-18
: PRIOR FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: 60/406,296
: PRIOR FILING DATE: 2002-08-27
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 24
: LENGTH: 400
: TYPE: PRT
: ORGANISM: RAT FOX Q1
US-10-650-112-24

Alignment Scores:
Pred. No.: 4.77e-65 Length: 400
Score: 1534.00 Matches: 311
Percent Similarity: 79.90% Conservative: 15
Best Local Similarity: 76.23% Mismatches: 68
Query Match: 70.08% Indels: 14
DB: 16 Gaps: 7

US-10-087-080-31 (1-1209) x US-10-650-112-24 (1-400)

QY 1 ATGAAGTTGAGGAGTTCCTGCTCCGCGGCGCCAGGAGGAGGAGGAGGAGGAGTGAAGCTG 60
Db 1 MetLysLeuGluValPheValProArgAlaIahISglYasPluMserGlySerAspLeu 20
QY 61 GAGGCGCGGCGGCGGAGCGAGCGCGCTGCCGCTGTGCGGCGGAGAGAGTCCCTG 120
Db 21 GluGlyAlaGlySerSerAspValProSerProLeuSerAlaIahISglYasPluSerLeu 40
QY 121 GGCTCAATGGGAGCTGCGCGGCC---AAGCGTCCGCGGCGGCGGCGGCGGAGATACG 177
Db 41 GlySerAspGlyAspCysAlaIahISglYasPluSerProAlaIahISglYasPluSerLeu 60
QY 178 CAG---GGCGAGCGGAGAGGAGTGCAGGAGGCGGCGGCGGCGGCGGAGGAGGAGGAGGAGG 234
Db 61 GluGlyGlyGlyGlyGluArgAsnSerSerGlyGlyProSerAlaIahISglYasPluSerCys 277

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QY 235 GCAGCAGCTGCTCCAGCGGTGTCGGGAGCGCGC-----GAGCCCGGGCGCGCGG 288
Db 78 -----AspProGluValThrAspGlySerArgThrGlnIleAspSerProValGly 93
QY 289 CCAGGCGCGGGGGCGCGCGGAGCGGCGGAGCGGCGCAGCAGCAGCCATTACCGCGCG 348
Db 94 ProGlyAlaGlySerValGlyGlyGlyGlyAlaArgSerIleProGlyThrArgArg 113
QY 349 CCCAGCCCCCTACTCTGATCATCGGCTCATGCGCATGCGCATCGCGCATCGCGCGG 408
Db 114 ProGlyProGlySerIleAlaAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 133
QY 409 GGGCGCTTACGCTGCGCGAGATCAAGATCACTCATGCGCAAGTTCCCTTTTCCGC 468
Db 134 GlyArgLeuThrLeuAlaGlnIleAlaGlnIleAlaGlnIleAlaGlnIleAlaGln 153
QY 469 GGCAGCTACAGCGGCGCGCGCACTCCGCGCGCGCAACACTTTCGTCACAGCTGCTTC 528
Db 154 GlySerIleThrGlyTyrArgAsnSerValArgGlnAsnLeuSerLeuAsnAspCysPhe 173
QY 529 GTCAAGGTGCTGCGCGCAGCCCTCGCGCGCTGCGCGCAAGCAACTACTGATGCTCAAC 588
Db 174 ValIysValLeuArgAspProSerArgProTyrGlyLysAspAsnTyrTyrMetLeuAsn 193
QY 589 CCCAACAGCGAGTACACTTTCGCGCAAGGGGTCTTTCGCGCGCGCGCGCAAGCGCTCAGC 648
Db 194 ProAsnSerGluTyrThrPheAlaAspGlyValPheArgArgArgGlySerLeuSer 213
QY 649 CAGCGCGCGCGGTCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 708
Db 214 HisArgThrThrValSerIleAspGlyLeuArgProGlnAlaIleProGlyProAla 233
QY 709 ---GCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCATGCGCGCGCGCG 765
Db 234 GlyThrProGlnProAlaProThrAlaGlySerSerProIleAlaArgSerProAlaArg 253
QY 766 CAGGAGGAGCGCGCAGCGCGCGCGCGCAAGTTCTTCAGCTCTTTCGCACTCAGCAGCATC 825
Db 254 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 273
QY 826 CTGGCGCAGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 885
Db 274 LeuSerIysProPheArgSerArgArgAspGlyAspProAlaLeuGlyValGlnLeuPro 293
QY 886 TGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 945
Db 294 TrpSerAlaAlaAlaProCysProProLeuArgAlaTyrProAlaLeuLeuProAlaSerSer 313
QY 946 TGCAGGGGCTGCTGCTGCTGCTGCGCGTACCGCGCGCGCGCGCGCGCGCGCGCG 1005
Db 314 GlyGlyAlaLeuLeuProLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 333
QY 1006 CGCGGAGCGCGAGGTGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1065
Db 334 ArgGlyAlaGlnIleValGlnProAlaAla---ProLeuLeuLeuAlaProLeuSerThrAla 352
QY 1066 GCGCGCGCGCGCAGCGCTCCGAGGCGCG---GCGCGCGCGCGCGCGCGCGCGCGCG 1122
Db 353 AlaProAlaLysProPheArgGlyProGlnThrAlaGlyAlaAlaAlaLeuLeuTyrCysPro 372
QY 1123 CTGGGCGCTGCGCGCAGCGCTTGCAGGCGCGCGCTTACGCGCGCGCGCGCGCGCG 1182
Db 373 LeuArgLeuProThrAlaLeuGlnAlaAlaAlaAlaAlaCysGlyProGlyProHisLeuSer 392
QY 1183 TACCGCGTGCAGCGCTCTAGCT 1206
Db 393 TyrArgValGlnThrLeuLeuAla 400

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RESULT 8
 US-10-205-823-136
 ; Sequence 136, Application US/10205823
 ; Publication No. US20030108963A1

```

; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gordatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Woneey, Angela M.
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR FILING DATE: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 465
; TYPE: prf
; ORGANISM: Homo sapiens
US-10-087-080-31 (1-1209) x US-10-205-823-136 (1-465)

Alignment Scores:
Pred. No.: 5,266-17 Length: 465
Score: 517.00 Matches: 157
Percent Similarity: 44.21% Conservative: 34
Best Local Similarity: 36.34% Mismatches: 132
Query Match: 23.62% Indels: 109
Db: 14 Gaps: 16

US-10-087-080-31 (1-1209) x US-10-205-823-136 (1-465)
QY 60 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 119
Db 39 GlyGlyGlyGlyGlyGlyProArgLeuAlaValPro----- 49
QY 120 GGGCTCAGATGGGAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 179
Db 50 -----AlaGlnArgArgArgArgArgSerTyrAla 60
QY 180 GGGGAGCGCGCAGAGAG-----TGC GGG 203
Db 61 GlyLysAspGlnLeuGlnAspLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
QY 204 AGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 263
Db 81 ProProAlaGlyGlySerProAlaProProGlyProAlaProAlaAlaGlyAlaGlyAla 100
QY 264 GGGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 323
Db 101 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 119
QY 324 ACGCAGCAGCATATATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 383
Db 119 AlysAsn---ProLeuVal-----LysProTyrSerIleAlaIleAlaIleThr 135
QY 384 CATGCCATCCGCGACCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 443
Db 135 IMetAlaIleLeuGlnSerProLysArgLeuThrLeuSerGlnIleCysGlnPheI 155

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Db      252 aAlaValProLysIleGluSerProAspSerSerSerSerSerLeuSerIleGlySer 272
QY      865 GCGCCCGGGA-----CGACGCTTCACT-----GAGGCGCC 894
Db      272 rProProGlySerLeuProSerAlaArgProLeuSerLeuAspGlyAlaAspSerAlaPr 232
QY      895 GCGCCCTGCGCGCGCGCTGCCCGGCTCCCGCTCTCCG----- 935
Db      292 oProPro-ProAla-----ProSerAlaProProProhiShiSerGlnGlyP 308
QY      936 -----CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 966
Db      308 heserValAspAsnIleMetThrSerLeuArgGlySerProGlnSerAlaAlaAlaGln 328
QY      967 TCGCGCTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1026
Db      328 eu-----SerSerIleLeuLeuAlaSerAlaAlaAlaSer 340
QY      1027 ACCGCGCC-----GCGCTCTCT----- 1043
Db      340 eArgAlaGlyIleAlaProProLeuAlaLeuGlyAlaTySerProGlnSerSerL 360
QY      1044 -----GCTTGACCTCTCCCGCGCGCGCGCGCGCGCGCGCG 1074
Db      360 euTySerSerProCysSerGlnThrSerSerAlaGlySerSerGlyGlyGlyGlyG 380
QY      1075 AAGCACTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1128
Db      380 lValGlyAlaAlaGlyGlyAlaGlyAlaGlyThrTyHisCysAsnLeuGlnAla 399
QY      1129 -----CTGCCCGCGAGCGCTG 1143
Db      400 MetSerLeuTyAlaAlaGlyGlnArgGlyGlyHisLeuGlnGlyAlaProGlyGlyAla 419
QY      1144 CAGGCGCGCTTACCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCG 1197
Db      420 GlYgIySerAlaValAspAspProLeuProAspTySerLeuProValThr 437

RESULT 10
US-10-007-280A-221
; Sequence 221, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Hervé
; APPLICANT: Salceda, Susana
; APPLICANT: Chenchua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,640
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patent version 3.1
; SEQ ID NO 221
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-007-280A-221

Alignment Scores:
Pred. No.: 3,39e-12 Length: 376
Score: 415.50 Matches: 128
Percent Similarity: 42.59% Conservative: 33
Best Local Similarity: 33.86% Mismatches: 118
Query Match: 18.98% Indels: 99
Db: 14 Gaps: 15

US-10-087-080-31 (1-1209) x US-10-007-280A-221 (1-376)
QY 232 CCGGAGAGAGCTGCTGCGAGCGGTGTGGCG-----GAGGCGCG 270

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Db      8 ProGluAspAlaAlaGlyAlaLeuLeuAlaProGluThrGlyArgThrValLysGlnPro 27
QY      271 GAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 330
Db      28 GlngIyProProProSerProGlyLysGlyGlyGlyGlyGlyGlyThrAlaProGlu 47
QY      331 AAGCATATACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 390
Db      48 lysProAspProAlaGln--LysProProTySerTyValAlaLeuAlaMetAla 66
QY      391 ATCCGCGACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 450
Db      67 lIeArgGluSerAlaGlnLysArgLeuThrLeuSerGlyIleTyGlnIleIleAla 86
QY      451 AAGTTCCTCTTTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510
Db      87 lysPheProPheTyGlnLysAsnLysGlyTyGlnAsnSerIleArgHisAsnLeu 106
QY      511 TCGCTCAACGACTGCTGTCAGAGGTGCGCGCGCGCGCGCGCGCGCG 570
Db      107 SerLeuAsnGluCysPheIleLysValProArgGlnGlyGlyGlyGly--ArgLysGly 125
QY      571 AACTATGATGACTCAACCCCAACAGCGAGTACACTTCGCGCGCGCGCG 630
Db      126 AsnTyTyTrpThrLeuAspProAlaCysGlnAspMetPheGlnLysLysnTyArgArg 145
QY      631 CCGCGCAAGCGCGCTAGCCCGCGCGCGCGCGCGCGCGCGCGCG 666
Db      146 ArgArgArgMetLysArgProPheArgProProProAlaHisPheGlnProGlyLysGly 165
QY      667 -----GCGCGCGCGCGCGCGCGCGCGCGCGAGAGAGCGCGCGCTCC-- 703
Db      166 LeuPheGlyAlaGlyGlyAlaAla--GlyGlyCysGlyAlaAlaGlyAlaGlyAlaAspG 185
QY      704 -----CCGCGCGCGCGCG----- 715
Db      185 YTyGlyTyLeuAlaProProLysTyLeuGlnSerGlyPheLeuAsnAsnSerTyPr 205
QY      716 -CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 771
Db      205 OleuProGlnProProSerProMetProTyAlaSerCysGlnMetAlaAlaAlaAla 225
QY      772 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 826
Db      225 aAlaAlaAlaAlaAlaAlaAlaAlaGlyProGlySerProGlyAlaAlaAlaValVa 245
QY      827 -----TGCGCAAGCGCTTCGCGCGCGCGCGCTCAGGAGACAGG-- 865
Db      245 lLysGlyLeuAlaGlyProAlaAlaSerTyGlyProTyThrArgValGlnSerMetAl 265
QY      866 -CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 915
Db      265 AleuProProGlyAlaValaAsnSerTyAsnGlyLeuGlyGlyProProAlaAlaProBr 285
QY      916 GCGTTCGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 975
Db      285 oProProProhiSprohiSpro----- 292
QY      976 GCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAGTGCCACCGACCGCGCG 1035
Db      293 -----HisProhiSAlaHisHis----- 298
QY      1036 CCGCTCTGCTTTCGACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1095
Db      299 -----LeuHis--AlaAlaAlaAlaAlaProProPro--AlaProProhiShiGly- 313
QY      1096 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1155
Db      314 -----AlaAlaAlaAlaProProProGlnGlnLeuS 323
QY      1156 GTCCGAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1205

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Db 67 ProlysAspLeuValIysProProIYserTyrIleAlaLeuIleThrMetAlaIleGln 86
 QY 397 GACTCGGCGGCGGCGGCTTGAAGCTGGCGAGATCAACGATACCTGATCCGAGCAATTC 456
 Db 87 AsnAlaProIuIuIysIleIleThrLeuAsnGlyIleTyrGlnPheIleMetAspArgPhe 106
 QY 457 CCCTTTTCCGCGGCGGAGCTACACGCGGTGGCGCAACTCCGTGGCGCAACAATTTCGCTC 516
 Db 107 ProPheTyrArgGlnuAsnIysGlnGlyTyrGlnAsnSerIleArgHisAsnLeuSerIleu 126
 QY 517 AACGACGCTTGTGCAAGGCTGCTGGCGGACCTCCGCGGCTTGGCGGCAAGCAACTAC 576
 Db 127 AsnGluCysPheValIysValIProArgAspAspIysIysPro---GlyIysGlySerTyr 145
 QY 577 TGGATGCTCAACCCCAACAGCGAGTACACTTCGCGGCGGCGGCTTTCGCGGCGGCGG 636
 Db 146 TrpThrLeuAspProAspSerTyrAsnMetPheGlnuAsnGlySerPheLeuArgArgArg 165
 QY 637 AAGCGCTTCAAGCCAGCGCGCGCGATCCCGCGCGCGGTGGCGGCGGCGGAGAGCGCGCG 696
 Db 166 ArgArgPheIysIysIysIysIysIysIysIysIysIysIysIysIysIysIysIysIys 181
 QY 697 GGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 753
 Db 182 HisLeuIysGlnuProProAlaIleSerIysGlyIleAlaProAlaIleThrProHisIleuAla 201
 QY 754 TCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 789
 Db 202 AspAlaProIysGlnuIleIuIysIysValIleIysSerGlnuIleAlaIleSerProAla 221
 QY 790 -----GGCAAGTTCTCCAGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 823
 Db 222 LeuProValIleThrIysValIleGlnuIleu---SerProGlnuSerAlaIleGlnuIleSerPr 241
 QY 824 -----TCCTGGCGAGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 879
 Db 241 OhrSerAlaIleIleSer---ThrProIleGlySerProAspIleSerLeuProGlnuHisIle 261
 QY 880 CTTCAAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 924
 Db 261 AlaIle---AlaProAsnGlyLeuProGlnuIlePheSerValIleGlnuIleMetThrLeuArgT 280
 QY 925 GCGCTCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 984
 Db 280 HisSerProGlnuIleGlnuIleu----- 287
 QY 985 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1044
 Db 288 ---SerProGlnuIleGlnuIleGlnuIleValIleProProLeuAlaIleuProTyrAla 306
 QY 1045 CTTGACCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1104
 Db 307 AlaIleIlePro---ProIleAlaIleTyrGlnuIleProCysAlaGlnuIleGlnuIleAlaIle 325
 QY 1105 GCGCAGCTGTAC---TGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1128
 Db 326 AlaGlyGlyTyrGlnuIleSerMetArgIleMetSerLeuTyrThrGlyAlaGlnuIlePro 345
 QY 1129 -----CTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1173
 Db 346 AlaHisMetCysValProProAlaIleuAspGlnuIleuSerAspHisProSerGlyPro 365
 RESULT 15
 US-09-963-285-10
 ; Sequence 10, Application US/09963285
 ; Patent No. US20020090707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Enebeck, Sven
 ; APPLICANT: Kirook, Katarina
 ; APPLICANT: Rondahl, Lena
 ; APPLICANT: Wasserman, Wyeeth
 ; TITLE OF INVENTION: PROMOTER SEQUENCES

; FILE REFERENCE: 13425-042001
 ; CURRENT APPLICATION NUMBER: US/09/963,285
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: SE 0004102-0
 ; PRIOR FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: US 60/238,897
 ; PRIOR FILING DATE: 2000-10-10
 ; PRIOR APPLICATION NUMBER: SE 0003435-5
 ; PRIOR FILING DATE: 2000-09-26
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-963-285-10
 Alignment Scores:
 Pred. No.: 9,47e-11 Length: 501
 Score: 384.50 Matches: 127
 Percent Similarity: 45.86 Conservative: 39
 Best Local Similarity: 35.08 Mismatches: 118
 Query Match: 17.57% Indels: 78
 DB: Gaps: 15
 US-10-087-080-31 (1-1209) x US-09-963-285-10 (1-501)
 QY 259 GCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 309
 Db 27 AlaIleGlySerTyrGlyIleMetAlaIleSerProMetGlyValIleTyrSerGlyHisProGlnu 46
 QY 310 -----AGCGGCGAGGCTGACAGCGAGCCATATACCGCGCGCGCGCGCGCGCGCGCG 351
 Db 47 GlnTyrSerAlaGlyMetGlyArgSerTyrAlaProTyrHisIleHisIleGlnuProAlaIle 66
 QY 352 -----AAGCGCGCTTACTGATCATCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 396
 Db 67 ProlysAspLeuValIysProProIYserTyrIleAlaLeuIleThrMetAlaIleGln 86
 QY 397 GACTCGGCGGCGGCGGCGGCTTGAAGCTGGCGAGATCAACGATACCTGATCCGAGCAATTC 456
 Db 87 AsnAlaProGlnuIleIleThrLeuAsnGlyIleTyrGlnPheIleMetAspArgPhe 106
 QY 457 CCCTTTTCCGCGGCGGAGCTACACGCGGTGGCGCAACTCCGTGGCGCAACAATTTCGCTC 516
 Db 107 ProPheTyrArgGlnuAsnIysGlnuIleTyrGlnAsnSerIleArgHisAsnLeuSerIleu 126
 QY 517 AACGACGCTTGTGCAAGGCTGCTGGCGGACCTCCGCGGCTTGGCGGCAAGCAACTAC 576
 Db 127 AsnGluCysPheValIysValIProArgAspAspIysIysPro---GlyIysGlySerTyr 145
 QY 577 TGGATGCTCAACCCCAACAGCGAGTACACTTCGCGGCGGCGGCTTTCGCGGCGGCGG 636
 Db 146 TrpThrLeuAspProAspSerTyrAsnMetPheGlnuAsnGlySerPheLeuArgArgArg 165
 QY 637 AAGCGCTTCAAGCCAGCGCGCGCGGCTCCCGCGCGCGGCTGGCGGCGGAGAGCGCGCG 696
 Db 166 ArgArgPheIysIysIysIysIysIysIysIysIysIysIysIysIysIysIysIysIys 181
 QY 697 GGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 753
 Db 182 HisLeuIysGlnuProProAlaIleSerIysGlyIleAlaProAlaIleThrProHisIleuAla 201
 QY 754 TCGCCCGCGCGCGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 789
 Db 202 AspAlaProIysGlnuIleGlnuIysValIleIysSerGlnuIleAlaIleSerProAla 221
 QY 790 -----GGCAAGTTCTCCAGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 823
 Db 222 LeuProValIleThrIysValIleGlnuIleu---SerProGlnuSerAlaIleGlnuIleSerPr 241
 QY 824 -----TCCTGGCGAGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 879

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Db      241 cArgSerAlaAlaSer-ThrProAlaGlySerProAspGlySerLeuProGluHisIAsa 261
QY      880 CTTCAgTGGGGCGCGCGCCCTGGCCCGCGCTGCC-----CGCGTTCCCC 924
      ||::: ||||| ||||| :::
Db      261 lAlAla---AlaProAenGlyLeuProGlyPheSerValGluAsnIleMetThrIleuArgT 280
QY      925 GCGCTGCTCCCGCGCGCGCCCTGGCAAGGCGCTGCGGCTGCGCGGTACGCGCGGAGC 984
      ::::| ||||| |||||
Db      280 hSerProProGlyGlyIleu----- 287
QY      985 GAAGCGCGCGCGCTGGGCGCGCGCGAGGCCAGGTGCCACCGCGCGCGCCCTCTCTG 1044
      ::: ||||| ||||| ||||| |||||
Db      288 --SerProGlyAlaGlyArgAla-GlyLeuValIvalProProIleuAlaLeuProTyrAla 306
QY      1045 CTTGCACTCTCCCGCGCGCGCGCCCGCAAGCCACTCCGAGGCCCGCGCGCGCGCGC 1104
      ||||| ||||| ||||| ||||| :::|
Db      307 AlaAlaPro---ProAlaAlaTyrGlyGlnProCysAlaGlnGlyLeuGluAlaGlyAla 325
QY      1105 GCGCACCTGTAC---TGCCCGCGTGGCG----- 1128
      ||||| ||||| ::::|
Db      326 AlaGlyGlyTyrGlnCysSerMetArgAlaMetSerLeuTyrThrGlyAlaGluArgPro 345
QY      1129 -----CTGCCCGCGAGCCCTGGCAAGCGCGCGCTTAGTCCGNCGTCT--GGCCCG 1173
      :::| ||||| ||||| ||||| |||||
Db      346 AlaHisMetCysValProProAlaLeuAspGluAlaLeuSerAspHisProSerGlyPro 365
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Search completed: August 27, 2004, 15:59:01
Job time : 208.5 secs

2

Db 301 GCCCGCGGAGCAGC 314

RESULT 2
US-08-331-644-3
Sequence 3, Application US/08331644
Patent No. 5976872
GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,644
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1860 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-331-644-3

Query Match 15.5%; Score 187.6; DB 2; Length 1860;
Best Local Similarity 58.3%; Pred. No. 3.6e-22;
Matches 394; Conservative 0; Mismatches 264; Indels 18; Gaps 3;

QY 8 TGGAGGTGTTGCTCCCTCGCGCGCCCAACGAGGAGGAGTGCATCCGAGCGGCG 67
DB 421 TCGACGTGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 68 CGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 127
DB 481 GCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 540
QY 128 ATGGGAGCTGCGCGCGCCCAAGCGTCCGCGGCGCGCGCGCGCGAGATACGAGGCGAGC 187
DB 541 CTTACGCGCGGAGGAGTGCATC-----TGGAGGAGCTGAGAGAGAGAGAGAGC 588
QY 188 GCGAACAAGAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 247
DB 589 ATGACCTGCTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 648
QY 248 CAGCGGTGTGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 307
DB 649 CCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 708
QY 308 GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 367

Db 709 GTACGGGCGCGGAGCAGCGGCGGCGGCGCTACAGANTCCGCTGTGAAGCCGCCCTACTCGT 768
QY 368 ACATCGCGCTCATCCGCGCATATGCGCATCCGCGAGCTCCGCGGCGGCGGCGCTGAGCGCG 427
DB 769 ACATCGCGCTCATCCGCGCATATGCGCATCCGCGAGCGCCCAAGAGGCGCGCTGAGCGTACG 828
QY 428 AGATCAAGAGTACCTCATGGCGCAAGTTCCTCTTTTCCGCGGCGAGCTACAGCGGCTGCG 487
DB 829 AGATTCGCGAGTTTCAACAGACGCGCGCTTCCTTACTACCGGAGAGTTCGCCGCTTGGG 888
QY 488 GCAACTCCGTGCGCGCAACAACCTTTGCTDAGACGCTTTGTTGAAGTGTGCGGAGC 547
DB 889 AGAAGAGCATCGCTCACACTGTGCTCAACGACTGCTTCGTCAAGATCCCGCGGAC 948
QY 548 CCTCGGCGCGCTGGGCGAAGAGCAACTACTGATGCTCAACCCCAAGGAGTACACT 607
DB 949 ---CGGCGAACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1005
QY 608 TCGCGAGCGGAGTCTTCCGCGCGCGCGCGCGAGCGCTCAGCGAGCGCGGCGGCTCCCG 667
DB 1006 TCGACAGCGGAGGAGTCTTCCGCGCGCGCGCGAGCGCTTCA---AGCGCGAGCGCTACTCG 1062
QY 668 CGCGCGGCGCTGCGGCGC 683
DB 1063 ATCCCGCGCTGGGAGC 1078

RESULT 3
PCT-US93-04102-3
Sequence 3, Application PC/TUS9304102
GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04102
FILING DATE: 19930430
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1860 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-04102-3

Query Match 15.5%; Score 187.6; DB 5; Length 1860;
Best Local Similarity 58.3%; Pred. No. 3.ee-22;
Matches 394; Conservative 0; Mismatches 264; Indels 18; Gaps 3;

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QY      8 TGAAGTGTTCCTCCGCGCGCCACCGGAGCAAGCAGGCGAGTCACTGAGAGGCG 67
DB      421 TCAGCTGTGTGGGGAGGGGAGAGCAACAGAGAGAGAGAGATGACAGAGAGGCG 480
QY      68 CGGCGGCAAGCAGCGCCCTCCCGCTGTGCGCGCGGAGAGAGATCTCTTGGCTCAG 127
DB      481 GCGCGCGCCCGCGCGCGCGGCTCCCGGTTTCCAGCTCGAGCCCGAGCGAGGCGT 540
QY      128 ATGGGAGCTGCGGGGCAAGCCGCTCCGCGGCGCGCGCGCGAGATCCGCGAGAGCTGCTG 247
DB      541 CTTACGCGGGGAGGTGATC-----TCAGAGACTGAGAGAGAGAGAGAGACG 588
QY      188 GCGAGAGAGTGCAGAGAGCGCGCGCGCGAGAGAGAGATCCGCGAGAGCTGCTG 247
DB      589 ATGACCTGTGCTGCGCGCGCGCGCGCGCGCTCCCGGCTCCGAGGCTTGGCGCG 648
QY      248 CAGCGGTGTGCGGAGGCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
DB      649 CCGCGGAGACGCGGCTGCGCGCGCTGACGCGCGCGAGAGCGAGCGCGCGCGAGGTG 708
QY      308 GAGAGCGAGAGGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
DB      709 GTACGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 768
QY      368 ACATCGCGCTCATCGCATAGCCATCGGAGCTCGCGCGCGCGCGCGCTTGAAGCTGCGCG 427
DB      769 ACATCGCGCTCATCGCATAGCCATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 828
QY      428 AGATCAAGAGTACCTCATAGGAGAGTCCCTTTTTCGCGCGAGCTACAGCGGCTGCG 487
DB      829 ACATCGAGAGTTCATACAGAGAGCGCTTCTTACTACGCGAGAGAGTCCCGGCTTGGC 888
QY      488 GCAATCGGTGCGGCAACACCTTTGCTCAAGAGTCTTCTGTAAGAGTCTGCGGAGCC 547
DB      889 AGAAGAGATCCGTCAACAGCTGTGCTCAAGAGCTTCTGTAAGAGTCCCGGAGAG 948
QY      548 CCTCGCGGCTTGGGCAAGAGCAACTGATGATCAACCGCAACAGAGTACACT 607
DB      949 ---CGGAGAACCGCGGCAAGGCAACTATGAGAGCTGCAAGAGTCCGAGATATGT 1005
QY      608 TGGCGGAGCGGCTTTTCGCGCGCGCGCGAGCGCTTACGCAAGCGCGCGGCTCCCG 667
DB      1006 TCGAAGAGCGGAGCTTCTGCGCGCGCGAGAGCGCTTCA---AGCGCGAGCGGTAAGT 1062
QY      668 GCGCGGCGCTGCGGC 683
DB      1063 ATCCCGCGCTGCGGAGC 1078
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RESULT 4
US-09-220-132-21

; Sequence 21, Application US/09220132
; Patent No. 6506807
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; FILE REFERENCE: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/220,132
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1965
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-220-132-21

Query Match 15.3%; Score 184.4; DB 4; Length 1965;
Best Local Similarity 54.4%; Pred. No. 1.2e-21;
Matches 492; Conservative 0; Mismatches 386; Indels 26; Gaps 5;

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QY      278 GGGGCGGAGGAGCGAGCGCGCGCGCGCGAGCGCGAGAGGATGACGAGAGAGCAT 337
DB      116 GCGCGGCGCGCGCGCGCGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 175
QY      338 ATAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 397
DB      176 TCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 235
QY      398 ACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 457
DB      236 GCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 295
QY      458 CTTTTCGCGCGAGCTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 517
DB      296 CTTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 355
QY      518 AGGAGTCTTCTGTAAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 577
DB      356 AGGAGTCTTCTGTAAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY      578 GATGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 637
DB      413 GATGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
QY      638 AGCGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 694
DB      473 GCGGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 532
QY      695 CGGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 754
DB      533 TGGGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 592
QY      755 CGCGCGCG-----CGCGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 808
DB      593 CGCTGCGTCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652
QY      809 TGGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
DB      653 AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 712
QY      869 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 922
DB      713 CGCATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 772
QY      923 CGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 982
DB      773 CGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 832
QY      983 GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1034
DB      833 GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 892
QY      1035 GCGCGCTTCTGTAAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1094
DB      893 CGAGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 952
QY      1095 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1154
DB      953 CCGTACCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1012
QY      1155 AGTC 1158
DB      1013 ACTC 1016
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RESULT 5

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US-09-083-351-1
Sequence 1, Application US/09083351
Patent No. 6087107
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patil, Shiva
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
TITLE OF INVENTION: TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HONG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-May-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UTA-029.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 475..2133
US-09-083-351-1

Query Match 14.5%; Score 175.6; DB 3; Length 3946;
Best Local Similarity 50.1%; Pred. No. 2.9e-20;
Matches 552; Conservative 0; Mismatches 534; Indels 16; Gaps 4

23 CTCGCGCGGGCCCAAGCGGGGACAGCAGGCGAGTGTGAGAGGGCGCGGGCGCGCAGCGAGG 82
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372 CTCGCGCGGGCCCGGACCTGCGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGG 431
83 CGCCGTCGCCGCTGTCTGCGCGCGCGGAGAGACTCCCTCGGCTCAGATGGAGACTGCGCGG 142
432 GTGGGGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 490
143 CCAAGCGCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 202
491 CGGTGTCGAGCCCACTCCCTGAGGAGTGTGCTTACTTCGGCGGGCGAGAGGCTACT 550
203 GAGGCGGGGGCGGGCGCGGAGAGGAGCGATCCCGGACAGCTGTGAGCGAGTGTGAGCGG 262
551 ACCGCGCGGGCGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 610
263 AGGGCGCGAGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 322
611 TGTACTCTCGACCTTGCGACGCGGACAGTACCCGGGGGAGCATGGCCCGGCTTACGGGC 670
323 CACGACGACGACCATATACGGGGCGGGCC-----AAGCCCGCTACTGTACTAGCGCG 376

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Db	671	CTTACACGCCGACGCCGACGCCCAAGGAATGATGTGAAGCGCCCTTATAGCTATCGCGC	730
QY	377	TCATCGCCATGAGCCATTCGCGACTCGGCGGCGGCGCTTACGCTGGCGGAGATCAAGC	436
Db	731	TCATCAACCAATGGCCATTCAGAAAGCGCCCCGAGACAAGAAATCACTCGAACGGCATCTACC	790
QY	437	AGTACTCTATGGGCAAGTTCCTTTTTCGCGCGAGCTACAGCGGCTGGCGCAATCCG	496
Db	791	AGTTCAATCAAGAACCGTTCTCCCTTCTTACCGGAGCAACAAGCAGGAGTGGCAGAACGA	850
QY	497	TGGGCCAACACTTTCGCTCAACGACTGCTTCGTCAGAGTGCTGCGCGAACCCCTCGCGC	556
Db	851	TCGGCCAAACCTCTCGCTCAAGAGTGTCTTCAAGTGCGTCCAGCGCGGAGACAAGAGC	910
QY	557	CTGGGGGCAAGACAACATCTGATGTCTCAACCCCAACGCGAGTACCTTGGCCGACG	616
Db	911	C---GGCCAAAGGAGACTTGAACGCTGAGCCCGGACCTCTTCAACATGTTGAGAGACG	967
QY	617	GGGCTTCGCGCGCGCGCGCAACGCGCTCAAGCAGCGCGCGCGCGCGCGCGCGCGCGC	676
Db	968	GCACTTCTCGCGCGCGCGCGCGCTTCAAGAAAGAAAGACGCGGTAAAGAACAGAGAG	1027
QY	677	TGCGGCGCCGAGAGAGCC-----CGGAGCTTCCCGCGCGCCCGCGCGCGCGCGCGC	730
Db	1028	AGAAAGACAGGCTGCACTTCAAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1087
QY	731	CCCCGGGCTCGCGCGCGCATGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	790
Db	1088	CGCGGAGCAGGCGCGAGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1147
QY	791	GCAAGTCTCGAGTCTCTTGGCCATTCACAGCAATCCGCGCGCAAGCCCTTCGAGCGCGT	850
Db	1148	ACATCAAGACCGAGAAAGGTACGTGCGCCCTCGCGCGCGCGCGCGCGCGCGCGC	1207
QY	851	GCGTCAGAGGACACGAGCGCGCGCGAGACAGCTTCAGTGAGGCGCGCGCGCGCGCGC	910
Db	1208	CCCTGGGCGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1267
QY	911	TGCCCGCGTTCCCGCGGCTCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	970
Db	1268	GCAGCGTGTCCAGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1327
QY	971	CGTACGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1030
Db	1328	TGAGCGGTGCGGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1387
QY	1031	CGCGCGCGCGCTCTGTTGACCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGC	1090
Db	1388	GCGAGGCTTACGCGTGAACAATCATGACGTGCGCGGAGTCCGCGAGAGCGG	1447
QY	1091	CGGCGGCGCGGCGCGCGCGCGCCT	1112
Db	1448	CGCGGAGCTCAGCTCGCGCGCT	1469
RESULT 6			
US-09-083-352-1			
; Sequence 1, Application US/09083352			
; Patent No. 6207450			
; GENERAL INFORMATION:			
; APPLICANT: Sheffield, Val C.			
; APPLICANT: Alward, Wallace L. M.			
; APPLICANT: Stone, Edwin M.			
; APPLICANT: Nishimura, Darryl			
; APPLICANT: Patil, Shiva			
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS			
; TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR			
; NUMBER OF SEQUENCES: 22			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP			
; STREET: One Post Office Square			
; CITY: Boston			

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1659 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-083-351-3

Query Match 14.2%; Score 171.6; DB 3; Length 1659;
 Best Local Similarity 51.3%; Pred. No. 1.3e-19;
 Matches 483; Conservative 0; Mismatches 444; Indels 15; Gaps 3;

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QY 183 CGACGGCGAACAAGTGTGGGAGGCGGCGCGGAGAGGAGTCCCGGAGCAGC 242
Db 57 CGGCGCGAGCAAGCTACTACCGCGGCGCGCGCGCGCGCGGAGGCGGCTACACCG 116
QY 243 TGCTGACAGGTGTGGGAGGCGCGGAGGCGCGGCGCGCGGAGGCGGCGGCGG 302
Db 117 CATGCGGCGCGCGCGCGCTGTACTGTGACCGCTGCGACCGAGAGTACCGGCGG 176
QY 303 CGCGGGGAGCGGAGGCGGTGACGACGACGACCATATACGCGGCGGCGGCGGCGG 356
Db 177 CATGCGCGCGCGCGCGCTTACGCGGCGCTTACAGCGCGGAGCGCGGAGAGAGCC 236
QY 357 CCGCTACTGTACATCGCGCTCATCGCATGCGCATCGCGACTCGCGGCGGCGGCGCTT 416
Db 237 GCGCTTATGCTACATGCGCTCATACCATATGCGCATCAGAGAGCGCGCGGAGAGAT 296
QY 417 GAGCGTGGCGGAGATCAACGAGTACCTCATGGGAGAGTCCCGCTTTTCCGCGGAGCTA 476
Db 297 CACCGCTAAGAGGATCTACCAAGTTTCATGATGAGCGGCTTCCCTTCAACGCGGAGCAA 356
QY 477 CAGGGGCTGGCGGAGTCCGCTGCGGCGGAGGAGGAGTCTGCTGCTGCTGCTGCTGCT 536
Db 357 GCGAGGCTGGGAGGAGGAGTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 416
QY 537 GCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 596
Db 417 GCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 473
QY 597 CAGAGTACCTTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 656
Db 474 CTACAGATGTTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 533
QY 657 GCGGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 710
Db 534 CCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 593
QY 711 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 770
Db 594 CCGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 653
QY 771 GAGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 830
Db 654 GCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 713
QY 831 CAGAGCGCTTGTGCGAGGCGGTGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 890
Db 714 GCGCGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 773
QY 891 CCGCGCGCGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 950
Db 774 GAGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 833
QY 951 GCGCGCTGTGCGGCGGCTGTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1010
Db 834 GTGCGCGGCGGCGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 893
QY 1011 GCGCGAGGTGACACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1070

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Db 894 CCGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 953
QY 1071 CCGCAAGCCTCTCCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1112
Db 954 GGGGTGCGCGGAGGAGGCGGCGGCGGAGGCTCAGCTTCGCGCT 995

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RESULT 8
 US-09-083-352-3
 Sequence 3, Application US/09083352
 Patent No. 6207450

GENERAL INFORMATION:
 APPLICANT: Sheffield, Val C.
 APPLICANT: Alward, Wallace L.M.
 APPLICANT: Stone, Edwin M.
 APPLICANT: Nishimura, Darryl
 TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
 TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/083,352
 FILING DATE: 22-MAY-1998

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Arnold, Beth E.
 REGISTRATION NUMBER: 35,430
 TELEPHONE: 617-832-1000
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: UIA-029.01

TELEPHONE: 617-832-7000
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1659 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-083-352-3

Query Match 14.2%; Score 171.6; DB 3; Length 1659;
 Best Local Similarity 51.3%; Pred. No. 1.3e-19;
 Matches 483; Conservative 0; Mismatches 444; Indels 15; Gaps 3;

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QY 183 CGACGGCGAACAAGTGTGGGAGGCGGCGGAGAGGAGGAGTCCCGGAGCAGC 242
Db 57 CGGCGCGAGCAAGCTACTACCGCGGCGCGCGCGCGCGCGGAGGCGGCTACACCG 116
QY 243 TGCTGACAGGTGTGGGAGGCGCGGAGGCGCGGCGGCGGAGGCGGCGGCGGCGG 302
Db 117 CATGCGGCGCGCGCGCGCTGTACTGTGACCGCTGCGACCGCGAGAGTACCGGCGG 176
QY 303 CGCGGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 356
Db 177 CATGCGCGCGCGCTTACGCGGCGGCTTACAGCGCGGAGCGCGGAGGAGGAGGAGGAG 236
QY 357 CCGCTACTGTACATCGCGCTCATCGCATGCGCATCGCGACTCGCGGCGGCGGCGCTT 416
Db 237 GCGCTTATGCTACATGCGCTCATACCATATGCGCATCAGAGAGCGCGCGGAGAGAT 296

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QY	417	GAGCGTGGGGAGATCAACAGATGACTCATAGGGCAAGTTCCCTCTTTTTCGGCGGACGTA	476
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QY	477	CACGGGCTGGCGCAACTCCGTGGGGCCAAACCTTTGGCTTCAAGCATGCTGTTGCTCAAGT	536
Db	357	GCAGGGGTGGCAGAAACAGCATTCGGCCACAACCTCTGGCTCAAGAGTCTTGTCAGAGT	416
QY	537	GCTGGCGGACCCCTCGCGGCGCTGGGGGCAAGGACAACTACTGATGCTCAACCCCAACAG	596
Db	417	GCGCGCCGACGACAAAGAAAGCC---GGGCAAGGCACTTACTGAGCGCTGAGCCCGACCTC	473
QY	597	CGAGTACACTTGGCCGACGGGGTCTTTCCGCGCGCGCCGCAAGCGGCTTCAAGCAACCGCGC	656
Db	474	CTACCAACTGTTTCAGAAACGGCAGCTTCTTCGGCGGCGCGCGCGCTTCAAGAAAGAGA	533
QY	657	GCGGTCCTCCCGCGCGCGGCGCTGGCGGCCAGAGAGGCC-----CGGGCTTCCCGCGCGC	710
Db	534	CGCGGTGAAGAGACAAAGAGAAAGAAAGAACAGGCTGACCTTCAAGAAAGAACCGCCCGCGCGG	593
QY	711	CCCGCGCCCGCGCGCGCGCGCGCGCTCGCCCGGCATAGCGGTGGCCCGCGCGCGCAGAGA	770
Db	594	CCGCGAGCCCGCGCGCGCGCGCGCGCGCGAGAGAGCGCCACAGGCAACGCGCCGGTCCGAGCGC	653
QY	771	GGAAGCGCGCAAGCCCCCGCGGCAAGTTCTTCAGCTCTTTCGCATTCAGCAGCATCCGTGG	830
Db	654	GCGCGCCGTGGCCATTCAGAGCATCAAGACCCAGAAACGGTACGTGGCCCTTCGCGCGCCCA	713
QY	831	CAAGCCCTTCCGCGAGCGCTCGGCTCAGGGACACAGCGCCCCCGGGAAGACGCTTCAAGTGGG	890
Db	714	GCCCTGTCTCCCGCGCGCGCGCGCTTGGGACGCGGACAGCGCGCGCGCGGTCGCCAATGCA	773
QY	891	CGCGGCGCCCTGACCGCGCGCTGCCGCGTTCGCCGCGCGCTCTCCCGCGGGCGSCCTTGCAG	950
Db	774	GAGCCCGACAGCAACAGACAGACAGCTGTTCAGCGGGAAGACAGCCCCCGGGGACGCTTACC	833
QY	951	GCGCTTGCTGCGCTCTGCGCGGTACGGCGCGGCGACAGCGCGCGCGCTGAGGCGCGCGCA	1010
Db	834	GTGGCGCGGCGGCTCAAGCTTGAACGGTGGGATTCCCGCGCGCGCGCGCGCGCGCTTC	893
QY	1011	GCGCGAGGTGCACACCGACCGCGCGCGCCCTCTCTGTTGACCTTCTCCCGGCGGGCGCCC	1070
Db	894	CGCCCGCGCGCGCAACATAGCCAAAGGCTTTCAGCGTGAACAACATCATGAGCTGCTGGCG	953
QY	1071	CGCCAAAGCACTCCGAGGCGCGCGCGCGCGCGCGCGCGCAAGCT	1112
Db	954	GGGGTCGCGCAGAGCGCGCGCGCGAGCACTCAAGCTTCGGGCT	995

RESULT 9

US-07-882-292-1
Sequence 1, Application US/07882292
Patent No. 5324638
GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Esseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: c/o Cooper and Dunham, 30 Rockefeller
STREET: Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:

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1  APPLICATION NUMBER: US/07/882,292
2  FILING DATE: 19920513
3  CLASSIFICATION: 514
4  ATTORNEY/AGENT INFORMATION:
5  NAME: White, John P
6  REGISTRATION NUMBER: 28,678
7  REFERENCE/DOCKET NUMBER: 41472
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 212-977-9550
10 TELEFAX: 212-664-0525
11 TELEX: 422523 COOP UI
12 INFORMATION FOR SEQ ID NO: 1:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 2830 base pairs
15 TYPE: NUCLEIC ACID
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: cDNA
19 HYPOTHETICAL: N
20 ANTI-SENSE: N
21 FEATURE:
22 NAME/KEY: CDS
23 LOCATION: 443..1882
24 OTHER INFORMATION:
25 FEATURE:
26 NAME/KEY: misc feature
27 LOCATION: 926..1855
28 OTHER INFORMATION: /note= "nucleotide sequence encoding DNA"
29 OTHER INFORMATION: binding domain homology"
30 NAME/KEY: misc signal
31 LOCATION: 1883..1885
32 OTHER INFORMATION: /note= "translation termination codon"
33
34 US-07-882-292-1

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Query Match	12.6%	Score 152.8;	DB 1;	Length 2830;
Best Local Similarity	52.8%	Pred. No. 1.3e-16;		
Matches 409; Conservative	0;	Mismatches 347;	Indels 18;	Gaps 3;

QY	82	GGCGCTTCCCGCTGTCTCGGCGCGGAGACGACTCTCTTGAGGTCAAGATGGGACCTTGCGCG	141
Db	674	GCCCCGACGCCCCCGACGCGCGCGGCCCCACGACGAGCGGACGACGAACGAAAGGCCCCCAG	733
QY	142	GCCAAAGCCGATCCGCGGGGCGGCGGCCACAGAGATACGACAGGGGACGGCGCAACAGATGGCG	201
Db	734	CCGCTTTCGTCTCCGCGCTCCGCGCTCTTGAGCGGGGCCAAAGCTGACGCACTTTGAGGCC	793
QY	202	GGAGCGCGGCGGCGCGGAGAGAGCAGATCCCGGACGACGTCTGTCAAGCGGTGGTGCGG	261
Db	794	AAAGGCGAGCCAGCGGCGGCGCTGCGGAGGTGGCGCCCTGTGGGCGCGGACGAGAAAGAG	853
QY	262	GAGGCGCCGAGAGCGCGGGGCGGCGGCCGACAGCGCGGCGCGCGGAGCGCGAGCGT	321
Db	854	AAAGGCGCGGCGCTGAGGAGGAGAGAAAGAGGGGCGGCGCGGCAAGAGCGGG	913
QY	322	GCAAGCGCAAGCCATATACGCGCGGCGCC-----AAGCCCGCCCTACTGTGATC	369
Db	914	GAGGGGGGCAAGAGGGCGCACAGAAACAAGCGGCAAGTACGAGAGACCCCGCTTACTTAC	973
QY	370	ATGGCGCTCATCGCCATGCGCCATCCGCGACTCGGCGGGCGGCGCTTGACGCTGACGAG	429
Db	974	AAGCGCTCATCATGATGCGCCATCAGGACAGAGTCCCGAGAAAGCGCTGACGCTCAACGGC	1033
QY	430	ATCAAGAGATACCTCATATGGGCAAGTTCCCTTTTCCGCGGACAGTACAAGGCGTGGCGC	489
Db	1034	ATCTACAGATTATCAAGAAAGAACTTCCCTTACTACCGCGGAAACAACAGAGGCTGGCAG	1093
QY	490	AACTCGGTGCGCAACAACCTTTGGCTCAAGACTGCTTGGCAAGGTGCTCGGGAAGCC	549
Db	1094	AACTCATCGGCAACAACCTGTCCCTCAACAAGTGTCTGTGAAGGTACCGGCACTAC	1153
QY	550	TGCGGCGCTGAGGGGCAAGGACACTATGATGCTCAACCCCAACGCGAGTACACTTC	609

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04102
FILING DATE: 19930430
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 443..1882
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: 926..1255
OTHER INFORMATION: /note= "nucleotide sequence encoding DNA
OTHER INFORMATION: binding domain homology"
NAME/KEY: misc signal
LOCATION: 1883..1885
OTHER INFORMATION: /note= "translation termination codon"
PCT-US93-04102-1

Query Match 12.6%; Score 152.8; DB 5; Length 2830;
Best Local Similarity 52.8%; Pred. No. 1.3e-16;
Matches 409; Conservative 0; Mismatches 347; Indels 18; Gaps 3;
QY 82 GGGCCGTCCTCCGCTGTCGCGCGCGGAGACGATCCCTGCGCTCAGATGCGGATGCGCG 141
Db 674 GCGCCGCGAGCCCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 733
QY 142 GCCAAGCCGTCCTCCGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 201
Db 734 CCGCTTCGCTCCGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 793
QY 202 GAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 261
Db 794 AAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 853
QY 262 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 321
Db 854 AAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 913
QY 322 GCAGCGAGCAAGCCATATACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 369

Db 914 GAGGCGGCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 973
QY 370 ATGCGGCTATCGCCATGCGCATCGCGAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 429
Db 974 AACGCGCTCATGATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1033
QY 430 ATCAAGAGTACCTCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 489
Db 1034 ATTTACGAGTTTATCATGAAGAACTTCCCTTACTACCGCGAGAAAGAGCGGCTGGCAG 1093
QY 490 AACTCGTGCGCCACCAACTTTTGGCTCAAGAGTCTTGGTCAAGGTCGCGCGCGCGCGCG 549
Db 1094 AACTCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1153
QY 550 TCGCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 609
Db 1154 GACGACCC--GCGCAAGGCGCAACTTCTGATCTGACCGCGCGCGCGCGCGCGCGCGCG 1210
QY 610 GCGGAGGCGGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 669
Db 1211 ATCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1270
QY 670 CCGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 729
Db 1271 TTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1327
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Db 1328 TCCCTTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387
QY 790 GCGAAGTCTCAGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 843
Db 1388 TTGAGTTACAGGAGCACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1441

RESULT 12
US-09-976-594-927
Sequence 927, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Fumess, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 927
LENGTH: 1309
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Inocyte ID No. 6673549 3687719CB1
US-09-976-594-927

Query Match 11.1%; Score 134.6; DB 4; Length 1309;
Best Local Similarity 57.6%; Pred. No. 1e-13;
Matches 261; Conservative 0; Mismatches 189; Indels 3; Gaps 1;
QY 340 ACGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 399
Db 93 ACTAGCAACCAAGCCCTCCCTCAGCTACATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 152
QY 400 TCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 459
Db 153 TCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 212
QY 460 TTTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 519

DB 213 TTCTACCGCAACCGCGCCGCTGGCGAAGACAGATCCGCCACAATCTGTCACTCAAC 272
QY 520 GACTGCTTCGTCAAGGTGTGTGCGGACCCCTCGCGCCCTGGGGCAAGCAACTACTG 579
DB 273 GAGTGGTTTGTCAAGGTGTGCCCCGATGACCGCAAGCC---AGGCAAGGGCAGCTACTG 329
QY 580 ATGCTCAACCCCAAGCGGAGTACACTTTCGCCAGAGGGGTCTTCGCCCGCGCGCGCAAG 639
DB 330 AGCTGGACCTTGACATGCGCAGCAGCATGTTTGAAGCAGGAGCTTCTTACGCGCGCGC 389
QY 640 CGCTTCAGCGCAGCGCGCGCGGTCCCGCGCCGCTGCGCGCGCGCAAGAGCGCCCGGCG 699
DB 390 CGCTTACCCCGAGACAGAGTGTGTAGGGGACCCGGGGCCCGCAAGGAGCGCGTGA 449
QY 700 CTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 759
DB 450 CCCCTCAGGGGCGCGCAGCGAGGAGCGAGTCTCCCAAGCGCAAGCGCGCAGGAGTGC 509
QY 760 GCCCGCAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 792
DB 510 TCATTCCACAGAGCTGCCAGATCCCAAGGCG 542

RESULT 13
US-08-331-644-4
Sequence 4, Application US/08331644

GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,644
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-331-644-4

Query Match 10.8%; Score 130.2; DB 2; Length 1155;
Best Local Similarity 67.5%; Pred. No. 5,1e-13;
Matches 199; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

QY 352 AAGCCCCCTACTCGTACATCGCGCTCATGCGCATGCGCATTCGCGAGCTCGCGGCGG 411
DB 499 AAGCGCCCTTACAGCTATATAGCGCTCATACCATGCGATCGAAGCCGCGCAGAGAG 558
QY 412 CGCTTGACGCTGGCGAGATCAAGAGTCCATGCGGCAAGTTCCCTTTTCGCGGCG 471
DB 559 AAGATCATCTTAAGCGCATTAACGATTCATATGAGACCGTTTCCCTTCTTACCGCGAG 618
QY 472 AGCTACAGCGGCTGGCGCAACTCCGTGCGCGCAACACTTTCGCTCAACGACTGCTGTG 531
DB 619 AACAGCAGGGCTTGCGAGAACAGATCCGCCCAACTGTCACTCAATGAGTGTCTGTG 678
QY 532 AAGTGTGCGGACCCCTCGCGGCGCTTGGGGCAAGCAACTACTGATGCTCAACCC 591
DB 679 AAGTGC CGCGGACGACCAAGAGCC---GGCGAAGGGAGCTTACGAGCGTGAACCG 735
QY 592 AACAGGATTAACCTTCGCCGAGCGGGGTCTTCGCCGCGCGCGCGCAAGCGCTCA 646
DB 736 GACTCTACAACTGTTGAGAAATGSCAGCTTCTCGCGCGCGCGCGCGCTTCA 790

RESULT 14
PCT-US93-04102-4
Sequence 4, Application PC/TUS9304102

GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04102
FILING DATE: 19930430
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-04102-4

Query Match 10.8%; Score 130.2; DB 5; Length 1155;
Best Local Similarity 67.5%; Pred. No. 5,1e-13;
Matches 199; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

QY 352 AAGCCCCCTACTCGTACATCGCGCTCATGCGCATGCGCATTCGCGAGCTCGCGGCGG 411
DB 499 AAGCGCCCTTACAGCTATATAGCGCTCATACCATGCGATCGAAGCCGCGCAGAGAG 558

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Db 301 GCGCGCGGAGAGCGGAGAGTGTGCGGAGCGGCGCGGAGAGAGCGATCCCGGAGCA 360
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Db 361 TACTGTACATGCGCTCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 420
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Db 421 CTGGCGGAGATCAAGAGTACCTCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 480
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Db 481 GCGTGTGCGAACTCCGTGTGCGCAAACTTTGCTCAAGCATGCTTGTGTGAGTGTG 540
QY 541 CGCGACCCCTGTGCGCGCTGTGCGGAGAGAGCACTACTGATGTCTCAACCCCAAGAGAG 600
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Db 541 CGCGACCCCTGTGCGCGCTGTGCGGAGAGAGCACTACTGATGTCTCAACCCCAAGAGAG 600
QY 601 TACACCTTGTGCGGAGAGAGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
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Db 601 TACACCTTGTGCGGAGAGAGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 661 GTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
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Db 661 GTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 721 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
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Db 721 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 AGCGCGCGGAGAGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
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Db 781 AGCGCGCGGAGAGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 841 CGGAGCGGTGTGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
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Db 841 CGGAGCGGTGTGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
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Db 961 CGCGCTGTGCGGAGAGAGTGTGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 1021 CCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
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Db 1021 CCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
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Db 1081 CTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
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Db 1141 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 CTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
|
|
|
Db 1201 CTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260

```

```

RESULT 2
US-10-274-177-9
; Sequence 9, Application US/10274177
; Publication No. US20040038225A1
; GENERAL INFORMATION:
; APPLICANT: MARKOMITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; FILE REFERENCE: CMW-P01-003
; CURRENT APPLICATION NUMBER: US/10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/10/229,345
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1161)..(1161)
; OTHER INFORMATION: n=a, c, g, or t
US-10-274-177-9

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Query Match          99.9%; Score 1208; DB 13; Length 1209;
Best Local Similarity 100.0%; Pred. No. 9,4e-247;
Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACCTTGTGAGAGTGTGCTGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
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|
|
Db 1 ATGACCTTGTGAGAGTGTGCTGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
QY 61 GAGGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
|
|
|
Db 61 GAGGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 GGTCTAGATGAGGAGACTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
|
|
|
Db 121 GGTCTAGATGAGGAGACTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GCGGAGCGCGAGAGAGTGTGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
|
|
|
Db 181 GCGGAGCGCGAGAGAGTGTGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 241 GGTGTGCGAGAGAGTGTGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
|
|
|
Db 241 GGTGTGCGAGAGAGTGTGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 GCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
|
|
|
Db 301 GCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 TACTGTACATGCGCTCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 420
|
|
|
Db 361 TACTGTACATGCGCTCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 420
QY 421 CTGGCGGAGATCAAGAGTACCTCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 480
|
|
|
Db 421 CTGGCGGAGATCAAGAGTACCTCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 480
QY 481 GCGTGTGCGAACTCCGTGTGCGCAAACTTTGCTCAAGCATGCTTGTGTGAGTGTG 540
|
|
|
Db 481 GCGTGTGCGAACTCCGTGTGCGCAAACTTTGCTCAAGCATGCTTGTGTGAGTGTG 540
QY 541 CGCGACCCCTGTGCGCGCTGTGCGGAGAGAGCACTACTGATGTCTCAACCCCAAGAGAG 600
|
|
|
Db 541 CGCGACCCCTGTGCGCGCTGTGCGGAGAGAGCACTACTGATGTCTCAACCCCAAGAGAG 600
QY 601 TACACCTTGTGCGGAGAGAGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
|
|
|
Db 601 TACACCTTGTGCGGAGAGAGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660

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; PRIOR APPLICATION NUMBER: 10/274,177
 ; PRIOR FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: 10/229,245
 ; PRIOR FILING DATE: 2002-08-26
 ; PRIOR APPLICATION NUMBER: 60/406,296
 ; PRIOR FILING DATE: 2002-08-27
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 25
 ; LENGTH: 1212
 ; TYPE: DNA
 ; ORGANISM: HUMAN FOXO1
 US-10-650-112-25

Query Match 97.7%; Score 1180.6; DB 17; Length 1212;
 Best Local Similarity 98.9%; Pred. No. 5.9e-241;
 Matches 1199; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

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QY 1 ATGAAGTTGAGAGTGTTCCTCTCGCGGCGCCACGAGGAGCAAGAGGAGTGAACCTG 60
Db 1 ATGAAGTTGAGAGTGTTCCTCTCGCGGCGCCACGAGGAGCAAGAGGAGTGAACCTG 60
QY 61 GAGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 61 GAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 121 GGCTCAGATGAGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 177
Db 121 GGCTCAGATGAGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 177
QY 121 GGCTCAGATGAGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Db 121 GGCTCAGATGAGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 178 CAGGCGGAGCGGCGGAGCAAGAGTGCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 237
Db 181 CCGGCGGAGCGGCGGAGCAAGAGTGCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 238 GAGGCTGCTGCAAGCGGTGTGCGGAGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCG 297
Db 241 GAGGCTGCTGCAAGCGGTGTGCGGAGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCG 300
QY 298 GCGGCGCGGCGGAGCGGCGGAGGAGTGCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 357
Db 301 GCGGCGCGGCGGAGCGGCGGAGGAGTGCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 358 CCTTACTCTGACTTGGCGGCTCATGCGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGG 417
Db 361 CCTTACTCTGACTTGGCGGCTCATGCGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 418 AGGCTGCGGAGAGTCAAGAGTACCTCATGAGGAGATTCCTTTTCGCGGCGAGCTAC 477
Db 421 AGGCTGCGGAGAGTCAAGAGTACCTCATGAGGAGATTCCTTTTCGCGGCGAGCTAC 480
QY 478 AGGCGGTGCGGCAACTCCGCTGCGGCGGAGCAACTCTTTCGCTCAAGAGTGTG 537
Db 481 AGGCGGTGCGGCAACTCCGCTGCGGCGGAGCAACTCTTTCGCTCAAGAGTGTG 540
QY 538 CTGGCGGAGACCTCTCGCGGCGGCGGCGGCGGAGAGCAACTCTGATGCTCAACCCCAAGC 597
Db 541 CTGGCGGAGACCTCTCGCGGCGGCGGCGGCGGAGAGCAACTCTGATGCTCAACCCCAAGC 600
QY 598 GAGTACACCTTTCGCGGAGGAGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 657
Db 601 GAGTACACCTTTCGCGGAGGAGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 658 CGGCTCCCGCGCGCGGCGGCTGCGGCGGCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCG 717
Db 661 CGGCTCCCGCGCGCGGCGGCTGCGGCGGCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCG 720
QY 718 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 777
Db 721 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 778 GCGAGCGGCGGCGGAGGTTCTCAAGCTCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 837
Db 781 GCGAGCGGCGGCGGAGGTTCTCAAGCTCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
  
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QY 838 TTCCGAGCGGTGCTCAGAGGAGACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 897
Db 841 TTCCGAGCGGTGCTCAGAGGAGACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
QY 898 CCTTGCCTGCGGCTGCGGCGGCTTCCCGCGGCTTCCCGCGGCGGCGGCGGCGGCGGCGG 957
Db 901 CCTTGCCTGCGGCTGCGGCGGCTTCCCGCGGCTTCCCGCGGCGGCGGCGGCGGCGGCGG 960
QY 958 CTGCGGCTGCGGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1017
Db 961 CTGCGGCTGCGGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1020
QY 1018 GTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1077
Db 1021 GTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1080
QY 1078 CCACTCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1137
Db 1081 CCACTCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1140
QY 1138 GCGCTGCGAGCGGCGGCTTATGTCGAGCGTCTTGGCGGCGGCGGCGGCGGCGGCGGCG 1197
Db 1141 GCGCTGCGAGCGGCGGCTTATGTCGAGCGTCTTGGCGGCGGCGGCGGCGGCGGCGGCG 1200
QY 1198 CTCTTACCTTGA 1209
Db 1201 CTCTTACCTTGA 1212
  
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RESULT 6
 US-10-650-112-26
 ; Sequence 26, Application US/10650112
 ; Publication No. US20040110712A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARKOMITZ, Sanford D.
 ; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
 ; FILE REFERENCE: CMW-P01-044
 ; CURRENT APPLICATION NUMBER: US/10/650,112
 ; CURRENT FILING DATE: 2003-08-26
 ; PRIOR APPLICATION NUMBER: 10/274,177
 ; PRIOR FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: 10/229,245
 ; PRIOR FILING DATE: 2002-08-26
 ; PRIOR APPLICATION NUMBER: 60/406,296
 ; PRIOR FILING DATE: 2002-08-27
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 26
 ; LENGTH: 1203
 ; TYPE: DNA
 ; ORGANISM: MOUSE FOXO1
 US-10-650-112-26

Query Match 64.6%; Score 781.6; DB 17; Length 1203;
 Best Local Similarity 81.2%; Pred. No. 1.6e-156;
 Matches 991; Conservative 0; Mismatches 200; Indels 30; Gaps 6;

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QY 1 ATGAAGTTGAGAGTGTTCCTCTCGCGGCGCCACGAGGAGCAAGAGGAGTGAACCTG 60
Db 1 ATGAAGTTGAGAGTGTTCCTCTCGCGGCGCCACGAGGAGCAAGAGGAGTGAACCTG 60
QY 61 GAGGCGGCGGCGGAGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 61 GAGGCGGCGGCGGAGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 121 GGCTCAGATGAGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 177
Db 121 GGCTCAGAGCGGAGAGTGTGAGGAGCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 178 CA---GAGCGAGCGGAGCAAGAGTGCAGGAGGCGGCGGCGGCGGCGGAGAGGCGGATCCG 234
Db 181 GAGGAGGCGGCGGAGAGGAGTTCAGAGTGGCGGCGGCGGCGGCGGCGGAGAGGCGGATCCG 240
  
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QY	235	GCACCACTGCTGACGCGGTGTGTGGCGGAGGCGCGAGAGCCGGGAGCGCGGGCCAGGC	234
Db	241	GCACACTATG-----ACAGCAGAACGCAAGGCTCTCCGGGCAAGGCGCTGC	285
QY	295	GCGGCGCGCGCGGAGAGCGCGGAGAGGTGCACGCGACGACCCATATACGCGCGGCCAAG	354
Db	286	GCGGCGCGCGTGGCGGCGGAGAGGCGCGCGCGACGAAGCCGTACAGCGCGCGCCAG	345
QY	355	CCCCCTTACTGTATCATCTGGCGCTCATGCGCATATGGCCATATCGCGCATCGGGGGGCGGCG	414
Db	346	CCCCCATCTCTCATGCTCTCATGCGCATGCGCATGCGCATGCGCATGCGCGGCGGAGCG	405
QY	415	TTTACGCTGCGGAGATCAACGAGTACTCATATGGGCAAGTTCCCTTTTTCGCGGAGC	474
Db	406	CTGACACTGCGCGGATCAACGAGTACTCATATGGGCAAGTTCCCTTTTTCGCGGAGC	465
QY	475	TACACGGGCTGGCGCACTCCGTGGCGCAACCTTTGCTCAACGACTGTTGTGTAG	534
Db	466	TACACGGGCTGGCGCACTCCGTGGCGCAACCTTTGCTCAACGACTGTTGTGTAG	525
QY	535	GTGCTGCGCGACCCCTGCGGCGCCGTGGGGGCAAGGCAACTATGTGATGCTCAACCCCAAC	594
Db	526	GTGCTGCGCGACCCCTGCGGCGCCGTGGGGGCAAGGCAACTATGTGATGCTCAACCCCAAC	585
QY	595	AGCGAGTACACTTTCGCGACGCGGGTCTTTCCGCGCGCGCGCAAGCGGCTTCAGCCACGC	654
Db	586	AGCGATATACCTTTCGCGACGCGGGTCTTTCCGCGCGCGCGCAAGCGGCTTCAGCCACGC	645
QY	655	GCGCGGCTTCCCGCGCGCGCGGTGTGGGCGCGAGAGAGTCCGGGCTTCCCGCGC---CC	711
Db	646	ACCAAGTCTCCGCGTCCGGGCTGGCGCGGAGGAAAGCCCAACCGCACTGCGCGGAC	705
QY	712	CGCGCGCGCGCGCGCGCGCGCGCGCGCTTCGCGCGCGCATGCGCTGCGCGCGCGCAAGAG	771
Db	706	CGCGCGCGCGCGCGCGCGCGCGCGCGCTTCTCCCGATGCGCGCTGCGCGGCTGCGCAAGAG	765
QY	772	GAGCGCGCAAGCCCGCGCGGCAAGTTCTCAAGTCTTTCGCTCATGACAGCATCTGTGCG	831
Db	766	GAGCGCTCAAGCCCTGCGAGCAAGTTCTTCAAGTCTTTCGCTCATGACAGCATCTGTGCG	825
QY	832	AAAGCCCTTCGGAAGCGGTGCGCTCAAGGAGACACGCGCGCGGAGCGAGGCTTCAGTGGGG	891
Db	826	AAAGCTTTTCGAGCGCGCGCGACGCGCACTGTGCTGTGGGGGTGCACTACCTGTGGGGC	885
QY	892	GCGCGGCGCTGCGCGCGCGCTGCGCGCGTCTCCCGCGCTCTCCCGCGCGCGCTGACAG	951
Db	886	GCGCGTCTCTGCGCGCGCGCTGCGCGCGTATCCCGGCTCTTCCCGGCGCGCGGTGG	945
QY	952	GCGCTGCTGCGCTGTGCGCGTACGCGCGCGGCGAGCGCGCGCGGCTGGCGCGCGAG	1011
Db	946	GCTGTGCTAACGCTGTGTGCTTACGCGCGACAGCGAGCTGTAGCTGTGCGCGCGAG	1005
QY	1012	GCGGAGGTGCCACGCGACGCGCGCGCGCGCTTCGCTTGTGACCTGTCCGCGCGCGCGCGCC	1071
Db	1006	ACCGAGGTG---CAACCGCGCGCGCGCGCTTCTGTGTGGGCGCGCTTTCACGCGGAGCTCA	1062
QY	1072	GCGAGCACTCCAGAGCGCGCG---CGAGCGCGCGCGCGCACTGTACTGCGCGCTTGTGG	1128
Db	1063	GCGAGCACTTCCAGAGTCCGAGACCGCGCGCGCGCGCACTGTACTGCGCGCTTGTAGCG	1122
QY	1129	CTGCCGCGACGCTTCGAGCGCGGCTTATGTTCGAGCGTCTGTGCGCGGCACTGTGTGTAACCG	1188
Db	1123	CTGCCACGCGCGCTTCAGGCGCGCGACGCGGCTTCCGAGTCCGACACTGTGCTTAACCG	1182
QY	1189	GTGGAGAGCGCTGTAGCTTGA	1209
Db	1183	GTGGAGACTGTGTAGCTTGA	1203

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? Publication No. US20040110712A1
? GENERAL INFORMATION:
? APPLICANT: MARKOWITZ, Sanford D.
? TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
? FILE REFERENCE: CMU-P01-044
? CURRENT APPLICATION NUMBER: US/10/650,112
? CURRENT FILING DATE: 2003-08-26
? PRIOR APPLICATION NUMBER: 10/274,177
? PRIOR FILING DATE: 2002-10-18
? PRIOR APPLICATION NUMBER: 10/229,245
? PRIOR FILING DATE: 2002-08-26
? PRIOR APPLICATION NUMBER: 60/406,296
? PRIOR FILING DATE: 2002-08-27
? NUMBER OF SEQ ID NOS: 27
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO: 27
? LENGTH: 1203
? TYPE: DNA
? ORGANISM: RAT FOXO1
? US-10-650-112-27

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Query Match	64.0%	Score 773.4	DB 17	Length 1203
Best Local Similarity	80.2%	Pred. No. 8	Se-155	
Matches 977	Conservative 0	Mismatches 217	Indels 24	Gaps 5
QY	1	ATGAAGTTGAGAGTGTTCGTCCTTCGCGCGGCCACACGAGGCAAGACAGAGGCAATGACCTG	60	
Db	1	ATGAATTTGAGGTAATTTGCCCCACGCGCAGACCCACGAGGCAAGATGAGCAATGACCTG	60	
QY	61	GAGGCGCGCGCGCGCAGCAGACGCGCCGTCCTTCCTGTCGCGGCGGGAAGAAGACTCCCTG	120	
Db	61	GAGGCGCGCGCGCAGCAGACGCGCCGTCCTTCCTGTCGCGGCGGGAAGAAGACTCCCTG	120	
QY	121	GGCTCAGATGAGGAGCTGCGCGCGCCAA---GCCGTCCCGCGCGCGCGCGCCAGAGATAACG	177	
Db	121	GGCTTCAGCGGAGACTGTGCAAGCCCAACAGCCCGCGCGCGCGCAAGGCGCCGTGGATCTG	180	
QY	178	CAGGCGCAGCGCGCAACAGAGTGCGGAGCGCGGCGCGGCGCGAGAGGCGATCCCGCA	237	
Db	181	GAGGCGCGCGCGCGCAGAGAGATTTGAGTGG-----CGGCGCGCAGCACTCCAA	228	
QY	238	GCACTGTGTGACGCGTGTGTGCGGAGGCGCCGGAAGCGCGGCGCGCGCGCGCGCGCG	297	
Db	229	GACGATCCCGAGGTAACCGATGAGCAGACGAGAGGCTTCCCGGTGGGCGTGGCGCG	288	
QY	238	GCGCGCGCGGAGAGCGAGGATGCAACGACGAAAGCCATTAACGCGCGCGCGCCAAAGCC	357	
Db	289	GCGACGCTGGCGCGGTGAGAGGCGCGCGCAGCAAGCCGTACACGCGCGCGCCAAAGCC	348	
QY	358	CCCTACTGTATCATGCGCGCTCATGCGCAATGCGCATCCGCACTCGGCGGCGCGCGCTTG	417	
Db	349	CCCTACTCTCATGCACTCATGCGCATGCGCATCCGCACTCGCGGCGCGAGCGCTTG	408	
QY	418	ACGCTGCGGAGATTAACGATACCTCATGAGCAAGTCCCTCTTTTCGCGCGCGCACTAC	477	
Db	409	ACGCTGCGCGAGATCAACGAGTACTCATGAGCAAGTCCCTCTTTTCGCGCGCGCACTAC	468	
QY	478	ACGGCTGCGCGCACTCCGCGCGCAGCAACCTTTGCTCAACGACTGCTGTCAGAGTG	537	
Db	469	ACGGCTGCGCGCACTCCGCGCGCAGCAACCTTTGCTGCTACAGACTGTTGTCAAGTG	528	
QY	538	CTGCGCGAACCCCTCGCGCGCTTGAGGAGCAAGCAACTATCTGATGCTCAACCCCAAGC	597	
Db	529	CTGCGCGAACCCCTCGCGCGCTTGAGGAGCAACTATCTGATGCTCAACCCCAAGC	588	
QY	598	GAGTACACTTTGCGCGAGCGGAGTCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG	657	
Db	589	GAGTACACTTTGCGCGAGCGGAGTCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG	648	
QY	658	CGGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	714	
Db	649	ACAGTCTCCGCAATCGGAGCTACGCGCGAGAGAGCCCAACCGGACCTGCGGAGACCCG	708	

QY 905 CGCCGCTGCCCCGCTTCCCGCGCTCTCCCGCGGCGCTTGCAGAGGCTCTGCTGCCGC 964
DB 1099 CGCGCGCTGCGCTTATCCCGCGCTCTCCCGGCTGTCCGAGGCTGCTGCTGCCGC 1158
QY 965 TCTGCTGCTTACGAGCGCGGCGAGCGCGGCTGAGGCGCGCGAGGCTGAGCGAG 1024
DB 1159 TCTGCTGCTTACGAGCGCGGCGAGCGCGGCTGAGGCGCGCGAGGCTGAGCGAG 1224
QY 1025 CGACCGCGCGCGCTCTCTGCTTGCACCTCTCCCGCGGCGGCGCGCGCAAGCTCTCC 1084
DB 1215 AGCCCGCGCGCGCTCTCTGCTTGCAGCGCTCTCCCGCGGCGGCGCGCGCAAGCTCTCC 1274
QY 1085 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1141
DB 1275 GAGGCTCGGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1334
QY 1142 TGCAGCGCGCGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1201
DB 1335 TGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1394
QY 1202 TAGCTTGA 1209
DB 1395 TAGCTTGA 1402

RESULT 9

US-10-027-632-231353/c
; Sequence 231353, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231353
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231353

Query Match 34.1%; Score 412.6; DB 13; Length 585;
Best Local Similarity 98.3%; Pred. No. 2.1e-78;
Matches 415; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 788 CGGCGCAAGTTCTCCAGCTCTCTTCCGCAATGACAGATCTCTGCGCAAGCCCTTCCGCAAGC 847
DB 585 CGGCGCAAGTTCTCCAGCTCTCTTCCGCAATGACAGATCTCTGCGCAAGCCCTTCCGCAAGC 526
QY 848 GTGCGCTTACGAGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 907
DB 525 GCGCGCTTACGAGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 466
QY 908 CGTGCCTGCGCTTCCCGCGCTCTCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967

DB 465 CGCTGCCCGCGGTTCCCGCGGCTCTCCCGCGGCGCTTGCAGAGGCTCTGCTGCCGCTCT 406
QY 968 GCGCGTACGCGCGCGGCGGAGCGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1027
DB 405 GCGCGTACGCGCGCGGCGGAGCGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 346
QY 1028 CGCGCGCGCGCGCTCTGCTTGCACCTCTCCCGCGGCGGCGCGCGCGCGCGCGCGCGCGCG 1087
DB 345 CGCGCGCGCGCGCTCTGCTTGCACCTCTCCCGCGGCGGCGCGCGCGCGCGCGCGCGCGCG 286
QY 1088 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1147
DB 285 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 226
QY 1148 GCGCGTACGCGCGCGGCGGAGCGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1207
DB 225 CGCGCTTACGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 166
QY 1208 GA 1209
DB 165 GA 164

RESULT 10

US-10-027-632-231353/c
; Sequence 231353, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231353
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231353

Query Match 34.1%; Score 412.6; DB 16; Length 585;
Best Local Similarity 98.3%; Pred. No. 2.1e-78;
Matches 415; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 788 CGGCGCAAGTTCTCCAGCTCTCTTCCGCAATGACAGATCTCTGCGCAAGCCCTTCCGCAAGC 847
DB 585 CGGCGCAAGTTCTCCAGCTCTCTTCCGCAATGACAGATCTCTGCGCAAGCCCTTCCGCAAGC 526
QY 848 GTGCGCTTACGAGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 907
DB 525 GCGCGCTTACGAGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 466
QY 908 CGTGCCTGCGCTTCCCGCGCTCTCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967
DB 465 GCGTGCCTGCGCTTCCCGCGCTCTCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 406
QY 968 GCGGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1027

RESULT 14
US-10-205-823-135
Sequence 135, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Monahan, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Monsey, Angela M.
APPLICANT: Zhao, Karen
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 135
LENGTH: 2487
TYPE: DNA
ORGANISM: Homo sapiens
US-10-205-823-135

Query Match 16.7%; Score 201.4; DB 15; Length 2487;
Best Local Similarity 52.1%; Pred. No. 8.1e-34;
Matches 574; Conservative 0; Mismatches 512; Indels 16; Gaps 5;

QY 83 CGCCGCTCCGCTGTGCGCGCGGAGAGACATCCCTGGGCTCAGATGGGAGCTGCGCG 142
DB 517 CGACGACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 576
QY 143 CC-AAGCCGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 200
DB 577 GCGGCGCTGTACGCGCGGAGAGACGAGCTGAGAGATCTGGAGAGAGAGAGAGAGAG 636
QY 201 GGGAGCGCGGCGGCGGCGGCGGAGGAGGAGTCCCGGAGAGCTGTGCAAGCGGTGCGC 260
DB 637 TGACATCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 696
QY 261 GAGAGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 320
DB 697 GCGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 753
QY 321 TGACGCGAGCAAGGAGATATAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 380
DB 754 CGCGGCTAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 813
QY 381 CGCATGCGCATCCCGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440
DB 814 CACTGTGCGCATCTCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 873
QY 441 CCTCATGGGCAAGTCCCTTTTTCGCGGCGGAGCTACACGCGGCGGCGGCGGCGGCGGCGG 500
DB 874 CATGAGCGGCGGCTTCCCTACTACCGGAGAGAGTCCCGGCGGCGGCGGCGGCGGCGGCGG 933

QY 501 CCACAACTTTCGCTCAACAGCTGCTTCGCAAGGTGCTGGGAGCCCTCGCGCCCTG 560
DB 934 CCAACACTTCGCTCAACAGCTGCTTCGCAAGGTGCTGGGAGCCCTCGCGCCCTG 990
QY 561 GGGCAAGGCACTACTGATGCTCAACCCCAAGAGAGTACCTTCGCGCGAGGGGT 620
DB 991 GGGCAAGGCACTACTGATGCTGAGCGTGGAGCCCGAGGTCCCGGAGATGTTCCACAAAGGAG 1050
QY 621 CTTCCGCGCGCGGCGGAGAGCGCTTCAAGCGGCGAGCGGCGGCGGCGGCGGCGGCGG 680
DB 1051 CTTCCGCGCGCGGAGAGAGCGCTTCAAGCGGCGAGCGGCGGCGGCGGCGGCGGCGG 1110
QY 681 GCGCGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 740
DB 1111 CGCGAGCTCTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1170
QY 741 GCGCGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 800
DB 1171 CGCGCGCGGCGGCTTTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1224
QY 801 CAGCTCTTCGCTGATGAGAGATCTTGCAGAGCCCTTCGAGCGCTGCGCTCAGGA 860
DB 1225 CGGCGCTTACGCGCTGCGCTACGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1284
QY 861 CAGGCGCGCGGAGAGAGAGCTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 920
DB 1285 CTTGCGCGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1344
QY 921 CCGCGCGCTCTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 980
DB 1345 GCGCGCGGCGGAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1404
QY 981 GCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1040
DB 1405 GCACCGGCT--CGGCGCGGCGGCTTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1462
QY 1041 CCGCTGACCTCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1100
DB 1463 GCGCGGCGGCGGCTTACGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1522
QY 1101 CGGCGGAGACCTGTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1160
DB 1523 AGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1582
QY 1161 NGCTCTGCGCGGCACTGTGCG 1182
DB 1583 TCGCCCTGCGGCTTCCGCGGTGG 1604

RESULT 15
US-09-968-007A-802
Sequence 802, Application US/09968007A
Publication No. US20040115625A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
FILE REFERENCE: 689290-71
CURRENT APPLICATION NUMBER: US/09/968,007A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,316
PRIOR FILING DATE: 2000-10-02

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 2, 2004, 16:45:04 ; Search time 96 Seconds

(without alignments)
2323.857 Million cell updates/sec

Title: US-10-087-080-32

Perfect score: 402

Sequence: 1 MKLEFVPPRAHSDKQGS...ALVRRGPHLSYVETLLA 402

Scoring table: Oligo

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 segs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1360453

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=firststep -SUFFIX=Oligo.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=humand40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pco -NORM=ext -HEA_SIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSPALOCK=100 -LONCLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

Issued Patents NA:
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2: /cg2_6/prodata/2/ina/5B.COMB.seq:*
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5: /cg2_6/prodata/2/ina/ECTUS.COMB.seq:*
6: /cg2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	32	8.0	320	4	US-09-833-381-1266
2	14	3.5	1309	4	US-09-976-594-927
3	12	3.0	1860	2	US-08-331-644-3
4	12	3.0	1860	5	PCT-US93-04102-3
5	10	2.5	780	4	US-09-252-991A-710
6	10	2.5	1155	2	US-08-331-644-4
7	10	2.5	1155	5	PCT-US93-04102-4
8	10	2.5	1488	4	US-09-252-991A-623
9	10	2.5	1614	4	US-09-616-289-45
10	10	2.5	1659	3	US-09-083-351-3
11	10	2.5	1659	3	US-09-083-352-3
12	10	2.5	1965	4	US-09-220-132-21

13	10	2.5	2561	4	US-09-616-289-48	Sequence 48, Appl
14	10	2.5	3946	3	US-09-083-351-1	Sequence 1, Appl
15	10	2.5	3946	3	US-09-083-352-1	Sequence 1, Appl
16	10	2.5	5207	4	US-09-858-664A-1	Sequence 1, Appl
17	10	2.5	5207	4	US-10-274-978-1	Sequence 1, Appl
18	10	2.5	5207	4	US-10-274-978-3	Sequence 3, Appl
19	10	2.5	6000	1	US-08-348-006B-6	Sequence 6, Appl
20	10	2.5	6000	2	US-08-800-825A-6	Sequence 6, Appl
21	10	2.5	6000	3	US-09-158-657-6	Sequence 6, Appl
22	10	2.5	6000	5	PCT-US94-10166-6	Sequence 6, Appl
23	10	2.5	6363	4	US-09-023-655-879	Sequence 6, Appl
24	10	2.5	12425	4	US-09-616-289-50	Sequence 879, App
25	10	2.5	68750	3	US-09-335-409-1	Sequence 50, Appl
26	10	2.5	68750	4	US-09-568-102-1	Sequence 1, Appl
27	10	2.5	68750	4	US-09-567-969-1	Sequence 1, Appl
28	10	2.5	68750	4	US-09-568-480-1	Sequence 1, Appl
29	10	2.5	68750	4	US-09-568-482-1	Sequence 1, Appl
30	10	2.5	68750	4	US-09-568-476-1	Sequence 1, Appl
31	10	2.5	68750	4	US-09-567-899-1	Sequence 1, Appl
32	10	2.5	71989	4	US-09-443-501A-2	Sequence 2, Appl
33	9	2.2	72	4	US-09-404-879A-304	Sequence 304, App
34	9	2.2	72	4	US-09-338-933-304	Sequence 304, App
35	9	2.2	72	4	US-09-215-681-304	Sequence 304, App
36	9	2.2	72	4	US-09-216-003A-304	Sequence 304, App
37	9	2.2	227	4	US-09-056-556-165	Sequence 165, App
38	9	2.2	227	4	US-09-072-596-165	Sequence 165, App
39	9	2.2	227	4	US-09-072-967-165	Sequence 165, App
40	9	2.2	299	4	US-09-072-596-251	Sequence 251, App
41	9	2.2	339	4	US-09-072-967-256	Sequence 256, App
42	9	2.2	399	4	US-09-325-932A-93	Sequence 93, Appl
43	9	2.2	400	4	US-09-056-556-179	Sequence 179, App
44	9	2.2	400	4	US-09-072-596-174	Sequence 174, App
45	9	2.2	400	4	US-09-072-967-179	Sequence 179, App

ALIGNMENTS

RESULT 1
US-09-833-381-1266
Sequence 1266, Application US/09833381
Patent No. 6672186
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1266
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc_feature
LOCATION: (1)...(320)
OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1266

Alignment Scores:

Pred. No.: 8,566-19
Score: 32.00
Percent Similarity: 97.83%
Best Local Similarity: 97.83%
Query Match: 7.96%
DB: 4
Gaps: 0

US-10-087-080-32 (1-402) x US-09-833-381-1266 (1-320)

Qy 220 ProValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProPro 239

DB 92 CCGGTCCCGCGCGGCTGCGCGCCGAGAGAGCCCGGCGCTCCCGCGCGCCG 151
QY 240 Pro-AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArg[nglu]Lar 259
DB 152 CCGCGCGCGCGCGCGCGCGCGCTGCGCGCCGATGCGCTGCGCGCCGCGAGAGAGCG 211
QY 259 gNAserProAlaGly 264
DB 212 CGCGAGCGCGCGGCG 227

RESULT 2
US-09-976-594-927
Sequence 927, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 927
LENGTH: 1309
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 3687719CB1
US-09-976-594-927

Alignment Scores:
Pred. No.: 0.00731 Length: 1309
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 4 Gaps: 0

US-10-087-080-32 (1-402) x US-09-976-594-927 (1-1309)

QY 118 LysProProTyrSerTyrTlleAlaLeuLleAlaMetAlaIle 131
DB 105 AAGCCTCCCTACAGCTACATGCGCCTTATGTATGCGCATC 146

RESULT 3
US-08-331-644-3
Sequence 3, Application US/08331644
Patent No. 5976872
GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,644
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1860 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-331-644-3

Alignment Scores:
Pred. No.: 0.516 Length: 1860
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.99% Indels: 0
DB: 2 Gaps: 0

US-10-087-080-32 (1-402) x US-08-331-644-3 (1-1860)

QY 167 ArgHisAsnLeuSerLeuAsnAspCysPheValIys 178
DB 900 CGTCACACCTGTGCTCAACGACTGCTTGTGTAAG 935

RESULT 4
PCT-US93-04102-3
Sequence 3, Application PC/TUS9304102
GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04102
FILING DATE: 19930430
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELE: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1860 base pairs

TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-04102-3

Alignment Scores:
Pred. No.: 0.516 Length: 1860
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.99% Indels: 0
DB: 5 Gaps: 0

US-10-087-080-32 (1-402) x PCT-US93-04102-3 (1-1860)

QY 167 ArgHisAsnIeuSerLeuAsnAspCysPheValIys 178
DB 900 CGTCAACCTGTGCTCAACGACTGCTTGTCAAG 935

RESULT 5
US-09-252-991A-710/c
Sequence 710, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 710
LENGTH: 780
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-710

Alignment Scores:
Pred. No.: 11.7 Length: 780
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.49% Indels: 0
DB: 4 Gaps: 0

US-10-087-080-32 (1-402) x US-09-252-991A-710 (1-780)

QY 240 ProAlaProAlaAlaProAlaSerProArg 249
DB 190 COTGCACGAGCGGCTCCAGCTTCTCCGCGT 161

RESULT 6
US-08-331-644-4
Sequence 4, Application US/08331644
Patent No. 5976872
GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
NUMBER OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,644
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-331-644-4

Alignment Scores:
Pred. No.: 16.9 Length: 1155
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.49% Indels: 0
DB: 2 Gaps: 0

US-10-087-080-32 (1-402) x US-08-331-644-4 (1-1155)

QY 118 LysProProTyrSerTyrIleAlaIle 127
DB 499 AAGCCGCCCTACAGCTATATAGCGCTCATC 528

RESULT 7
PCT-US93-04102-4
Sequence 4, Application PC/TUS9304102
GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
NUMBER OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04102
FILING DATE: 19930430
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41472A-PCR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCR-US93-04102-4

Alignment Scores:
Pred. No.: 16.9 Length: 1155
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.49% Indels: 0
DB: 5 Gaps: 0

US-10-087-080-32 (1-402) x PCR-US93-04102-4 (1-1155)

QY 118 lvsProProTyrSerTyrIleAlaIleu116 127
DB 499 AMGGCGCCCTACAGCTATATAGCGCTCATC 528

RESULT 8
US-09-252-991A-623
Sequence 623, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 623
LENGTH: 1488
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-623

Alignment Scores:
Pred. No.: 21.3 Length: 1488
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.49% Indels: 0
DB: 4 Gaps: 0

US-10-087-080-32 (1-402) x US-09-252-991A-623 (1-1488)

QY 240 ProAlaProAlaProAlaSerProArg 249
DB 1329 CCTGCACCGCGGCTCCAGCTTCTCCGCGT 1358

RESULT 9
US-09-616-289-45
Sequence 45, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1614)
US-09-616-289-45

Alignment Scores:
Pred. No.: 23 Length: 1614
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.49% Indels: 0
DB: 4 Gaps: 0

US-10-087-080-32 (1-402) x US-09-616-289-45 (1-1614)

QY 236 AlaAlaProProAlaProAlaPro 245
DB 532 GCCGCGCGCGCGCGCGCGCGCGCGCGCTCC 561

RESULT 10
US-09-083-351-3
Sequence 3, Application US/09083351
Patent No. 6087107
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patil, Shiva
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
TITLE OF INVENTION: TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-029.02

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-083-351-3

Alignment Scores:
Pred. No.: 23.6
Score: 10.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.49%
DB: 3
Gaps: 0

US-10-087-080-32 (1-402) x US-09-083-351-3 (1-1659)

QY 118 LysProProTySerTyrIleAlaLeuIle 127
Db 232 AAGCGCCCTATAGCTACATCGCGCTCATC 261

RESULT 11
US-09-083-352-3
Sequence 3, Application US/09083352
Patent No. 6207450
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patel, Shiva
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,352
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-029.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-083-352-3

Alignment Scores:
Pred. No.: 23.6
Length: 1659

Score: 10.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.49%
DB: 3
Gaps: 0

US-10-087-080-32 (1-402) x US-09-083-352-3 (1-1659)

QY 118 LysProProTySerTyrIleAlaLeuIle 127
Db 232 AAGCGCCCTATAGCTACATCGCGCTCATC 261

RESULT 12
US-09-220-132-21
Sequence 21, Application US/09220132
Patent No. 6506607
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 1965
TYPE: DNA
ORGANISM: Homo sapiens
US-09-220-132-21

Alignment Scores:
Pred. No.: 27.6
Score: 10.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.49%
DB: 4
Gaps: 0

US-10-087-080-32 (1-402) x US-09-220-132-21 (1-1965)

QY 118 LysProProTySerTyrIleAlaLeuIle 127
Db 190 AAGCGCCCTACTCTGACATCGCGCTCATC 219

RESULT 13
US-09-616-289-48
Sequence 48, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53

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SOFTWARE: FastSPQ for Windows Version 4.0
SEQ ID NO. 48
LENGTH: 2561
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
FEATURE:
NAME/KEY: CDS
LOCATION: (246)...(1895)
US-09-616-289-48

Alignment Scores:
Pred. No.: 35.4 Length: 2561
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.49% Indels: 0
DB: 4 Gaps: 0

US-10-087-080-32 (1-402) x US-09-616-289-48 (1-2561)

Cy 236 AlAlAProProAlAProAlAPro 245
|||||
783 GCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 812

RESULT 14
US-09-083-351-1
Sequence 1, Application US/09083351
Patent No. 6087107

GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patil, Shiva
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
TITLE OF INVENTION: TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Aitold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-029.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 475..2133
US-09-083-351-1

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Alignment Scores:
Pred. No.: 52.9 Length: 3946
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.49% Indels: 0
DB: 3 Gaps: 0

US-10-087-080-32 (1-402) x US-09-083-351-1 (1-3946)
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Db 706 AAGCCGCCCATAGCTACATCGCGTCAAC 735

RESULT 15
US-09-083-352-1
/ Sequence 1, Application US/09083352
/ Patent No. 6207450
/ GENERAL INFORMATION:
/ APPLICANT: Sheffield, Val C.
/ APPLICANT: Alward, Wallace L.M.
/ APPLICANT: Stone, Edwin M.
/ APPLICANT: Nishimura, Barry J
/ APPLICANT: Patel, Shiva
/ TITLE OF INVENTION: GLACOVIA THERAPEUTICS AND DIAGNOSTICS
/ TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FOLEY, HOAG & ELIOT LLP
/ STREET: One Post Office Square
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02109-2170
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/083,352
/ FILING DATE: 22-MAY-1998
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Arnold, Beth E.
/ REGISTRATION NUMBER: 35,430
/ REFERENCE/DOCKET NUMBER: UIA-029.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-832-1000
/ TELEFAX: 617-832-7000
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3946 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 475..2133
/ US-09-083-352-1

Alignment Scores:
Pred. No.: 52.9 Length: 3946
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.49% Indels: 0
DB: 3 Gaps: 0

US-10-087-080-32 (1-402) x US-09-083-352-1 (1-3946)
QY 118 LysProProTyRSeTyRtLeaLeuLe 127

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Db 706 AAGCGCGCCTATAGCTACATCGCGCTCATC 735

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GenCore version 5.1.6
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Perfect score: 402
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Database: Published Applications NA:
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	402	100.0	1209	13	US-10-229-345-9	Sequence 9, Appl
2	402	100.0	1209	16	US-10-274-177-9	Sequence 31, Appl
3	402	100.0	1209	17	US-10-087-080-31	Sequence 9, Appl
4	402	100.0	1209	17	US-10-650-112-9	Sequence 25, Appl
5	324	80.6	1212	17	US-10-650-112-25	Sequence 26, Appl
6	114	28.4	1203	17	US-10-650-112-27	Sequence 1814, Ap
7	114	28.4	1203	17	US-10-650-112-27	Sequence 23153,
8	114	28.4	1203	17	US-10-152-319A-1814	Sequence 1266, Ap
9	73	18.2	585	16	US-10-027-632-231353	Sequence 4735, Ap
10	73	18.2	585	16	US-10-027-632-231353	Sequence 24908, A
11	32	8.0	320	9	US-09-833-381-1266	Sequence 23708, A
12	14	3.5	477	10	US-09-918-995-4735	Sequence 138699,
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14	12	3.0	312	15	US-10-029-386-23708	Sequence 138701,
15	12	3.0	425	13	US-10-027-632-138699	Sequence 138703,
16	12	3.0	425	13	US-10-027-632-138700	Sequence 1045, Ap
17	12	3.0	425	13	US-10-027-632-138701	Sequence 135, App
18	12	3.0	425	13	US-10-027-632-138701	Sequence 4009, Ap
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23	12	3.0	425	16	US-10-027-632-138703	Sequence 3044, Ap
24	12	3.0	1056	15	US-10-029-386-10008	Sequence 6254, Ap
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26	12	3.0	2487	13	US-10-342-887-1045	Sequence 67449, A
27	12	3.0	2487	13	US-10-172-118-1045	Sequence 20740, A
28	12	3.0	2757	15	US-10-205-823-135	Sequence 16847, A
29	12	3.0	2757	15	US-10-437-963-4009	Sequence 24740, A
30	12	3.0	5181	12	US-09-968-007A-802	Sequence 8737, Ap
31	11	2.7	1452	17	US-10-437-963-83324	Sequence 20713, A
32	11	2.7	2190	17	US-10-437-963-91335	Sequence 20688, A
33	10	2.5	327	17	US-10-437-963-65338	Sequence 64737, A
34	10	2.5	366	9	US-09-960-352-3044	
35	10	2.5	441	9	US-09-960-352-6254	
36	10	2.5	516	17	US-10-437-963-67449	
37	10	2.5	519	16	US-10-393-840-750	
38	10	2.5	520	15	US-10-029-386-20740	
39	10	2.5	543	9	US-09-864-761-16847	
40	10	2.5	543	9	US-09-864-761-24740	
41	10	2.5	597	9	US-09-864-761-8737	
42	10	2.5	597	15	US-10-029-386-20525	
43	10	2.5	642	15	US-10-029-386-20525	
44	10	2.5	714	15	US-10-029-386-20688	
45	10	2.5	717	17	US-10-437-963-64737	

ALIGNMENTS

RESULT 1
US-10-229-345-9
; Sequence 9, Application US/10229345
; Publication No. US20040038220A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; CURRENT REFERENCE: CWRU-P01-003
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1161)..(1161)
; OTHER INFORMATION: n=a, C, G, or T
US-10-229-345-9

Alignment Scores:


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Db 301 GGGCGGGGGAGCGCGGAGGTGACAGGACAAAGCATATCGCGCGCCCAAGCCCC 360
QY 121 TySerIlyIleAlaIleuAlaMetAlaIleArgSerSerIlyGlyIlyArgLeuThr 140
Db 361 TACTCGTACATCGCGCTCATCGCATGCGCATCGCGAGCTCGGGGCGCGCTTGACG 420
QY 141 LeuAlaGluIleAsnGlyIlyLeuMetGlyIlySerPhePheArgIlySerIlyThr 160
Db 421 CTGGCGGAGATCAACGATACCTCATGTGGGAAGTCCCTTTTCCGGGAGCTACACG 480
QY 161 G1YTPArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValIlyValLeu 180
Db 481 GGCTGGGCAACCTCGCGCCCAACACTTCCTCAACAGACTGCTTCTGCAAGTGCTG 540
QY 181 ArgAspProSerArgProIlyProIlyIlyAspAsnIlyTrpMetLeuAsnProAsnSerGlu 200
Db 541 CGGACCCCTCGCGCGCTGAGGACAGGACAACTACTGAGTGTCAACCCCAACAGCGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgIlySerIlySerHisArgAlaPro 220
Db 601 TACACCTTGGCGGACGAGGAGTCTTCCCGCGCGCGAGAGGCTCAAGCCAGCGCGCG 660
QY 221 ValProAlaProGlyIlyLeuArgProGlyGluAlaProGlyIlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGCGCTGCGCGCGCGAGAGGCGCGCGCGCTCCCGCGCGCGCGCGCG 720
QY 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgIlyGluIlyAlaAlaPro 260
Db 721 GGCGCGCGCGCGCGCGCTGCGCGCGAGTGTGCTGCGCGCGCGCGAGAGGCGCGCGCG 780
QY 261 SerProAlaGlyIlySerPheSerSerPheAlaIleAspSerIleLeuArgIlySerProPhe 280
Db 781 AGCGCGCGCGGAGAGTTCAGCTCTTCCCATGACAGCATCTGCGCAAGCCCTTC 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyIlyThrIleGluIlyIlyAlaAlaPro 300
Db 841 CCAGAGCGCTGCGCTCAGGAGACAGCGCGCGCGGAGACAGCTTCAAGTGGGCGCGCGCG 900
QY 301 CysProProLeuProAlaPheProAlaIleuProAlaAlaProCysArgAlaIleuPro 320
Db 901 TCCCGCGCGCTGCGCGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCTGCGCG 960
QY 321 ProLeuCysAlaIlyIlyIlyAlaGlyIlyProAlaArgLeuGlyAlaArgIlyAlaIlyVal 340
Db 961 CGGCTCTGCGGTAGCGCGCGCGGAGCGCGCGCGCTGGCGCGCGAGCGCGAGGTG 1020
QY 341 ProProThrAlaProProLeuLeuAlaProLeuProAlaAlaAlaProAlaIlyPro 360
Db 1021 CCACGAGCGCGCGCGCTCTCTGCTTGCACCTCTCCCGCGCGCGCGCGCGCGCAAGCCA 1080
QY 361 LeuArgGlyProAlaAlaGlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIly 380
Db 1081 CTCGAGAGCGCGCGCGCGCGCGCGCGCGCTGCTGCTGCGCGCGCGCGCGCGCGCGCG 1140
QY 381 LeuGluAlaAlaIleuValArgArgProGlyProHisLeuSerIlyProValGluThrIleu 400
Db 1141 CTGCGAGGCGCGCTTGTCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 401 LeuAla 402
Db 1201 CTAGCT 1206

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RESULT 3
us-10-087-080-31

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; Sequence 31, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.

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; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colore
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-00084005
; CURRENT APPLICATION NUMBER: US/10/087,080
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: winged helix/forkhead transcription factor (HFH1)
; NAME/KEY: modified_base
; LOCATION: (1161)
; OTHER INFORMATION: n = 5, a, c or t
; US-10-087-080-31

Alignment Scores:
Pred. No.: 0 Length: 1209
Score: 402.00 Matches: 402
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-087-080-32 (1-402) x US-10-087-080-31 (1-1209)
QY 1 MetIlyLeuGluValPheValProArgAlaAlaHisGlyAspIlySerIlySerAspLeu 20
Db 1 ATGAAGTTGAGAGTGTCTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
QY 21 GluIlyAlaGlyIlySerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
Db 61 GAGGGGCGGGGCGGAGCGAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 GlySerAspGlyAspCysAlaAlaIlyProSerAlaIlyGlyIlyAlaArgAspThrGln 60
Db 121 GGCTCAGATGGGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 GlyAspGlyGluGlnSerAlaGlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIly 80
Db 181 GCGGAGCGGAGAGAGTGTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 241 GCTGCTGAGCGGTGTGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 101 GlyAlaGlySerGlyGluGlyAlaArgSerIlyProIlyThrArgArgProIlyProPro 120
Db 301 GGCGGGGAGGAGGCGGAGGTGCGAGCGCAAGCCATATACCGCGCGCGCGCGCGCGCG 360
QY 121 TySerIlyIleAlaIleuAlaMetAlaIleArgAspSerAlaGlyIlyArgLeuThr 140
Db 361 TACTCGTACATCGCGCTCATCGCATGCGCATCGCGAGCTCGGGGCGCGCTTGACG 420
QY 141 LeuAlaGluIleAsnGlyIlyLeuMetGlyIlySerPhePheArgIlySerIlyThr 160
Db 421 CTGGCGGAGATCAACGATACCTCATGTGGGAAGTCCCTTTTCCGGGAGCTACACG 480
QY 161 G1YTPArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValIlyValLeu 180
Db 481 GGCTGGGCAACCTCGCGCCCAACACTTCCTCAACAGACTGCTTCTGCAAGTGCTG 540

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QY 181 ArgAspProSerArgProTyrpGlyLysAspAsnTyrTrrMetLeuAsnProAsnSerGlu 200
Db 541 CGGACCCCTCGGGGCTGGGGGCAAGACACTACTGATGCTCAACCCCAACAGAGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgLysArgLeuSerHisArgAlaPro 220
Db 601 TACACCTTCGCCGACGGGGTCTTCGCCGCGCGCGAGAGGCTTCAGCCACCGCGGGCGG 660
QY 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGCGCGCGCGCGCGAGGAGCGCGCGCGCTCCCGCGCGCGCGCGCGCC 720
QY 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGluAlaArgAla 260
Db 721 GCGCGCGCGCGCGCGCGCGCTGCGCGCGCATGCGCTCGCGCGCGCGCGCGCGCGCGCC 780
QY 261 SerProAlaGlyLysPheSerSerSerPheAlaAlaAspSerIleLeuArgLysProPhe 280
Db 781 AGCCCGCGCGCGCAAGTTCTCCAGCTCTTCGCCATCGACAGCATCTGCGCAAGCCCTTC 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrrpGlyAlaAlaPro 300
Db 841 CGCAGCGCGTGCCTCAGAGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 900
QY 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
Db 901 TGCCCGCGCGCTGCGCGCGCTTCCCGCGCTCTCCCGCGCGCGCGCGCGCGCGCGCGCTG 960
QY 321 ProLeuCysAlaTyrGlyAlaGlyGluProAlaArgLeuGlyAlaArgGlyAlaGlyVal 340
Db 961 CCGCTGCGCGGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGTG 1020
QY 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaAlaProAlaLysPro 360
Db 1021 CCACCGACCGCGCGCGCGCGCGCGCTGCGCGCTCTCCCGCGCGCGCGCGCGCGCGCA 1080
QY 361 LeuArgGlyProAlaAlaGlyGlyAlaHisIleuTyrCysProLeuArgLeuProAlaAla 380
Db 1081 CTCGAGGCGCGCGCGCGCGCGCGCGCGCGCATCTGACTGCGCGCGCGCGCGCGCGCG 1140
QY 381 LeuGlnAlaAlaLeuValArgArgProGlyProHisIleuSerTyrProValGluThrLeu 400
Db 1141 CTGAGAGGCGCGCTTACGTCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 1200
QY 401 LeuAla 402
Db 1201 CTAGCT 1206

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OTHER INFORMATION: n is a,t,g or c
US-10-650-112-9
Alignment Scores:
Pred. No.: 0
Score: 402.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 17 Gaps: 0
US-10-087-080-32 (1-402) x US-10-650-112-9 (1-1209)
QY 1 MetLysLeuGlnValPheValProArgAlaAlaHisGlyAspLysGlnLysSerAspLeu 20
Db 1 ATGAAGTTGAGGAGTGTTCCTCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
QY 21 GluGlyAlaGlyLysSerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
Db 61 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyAlaArgAspThrGln 60
Db 121 GGCTCAGATGGGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 GlyAspGlyGluGlnSerAlaGlyGlyLysProGlyAlaGluGlnAlaAlaProAlaAla 80
Db 181 GCGCAGCGCGCAACAGAGTGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 240
QY 81 AlaAlaAlaAlaValValAlaGluGlyAlaGluAlaGlyAlaAlaGlyProGlyAlaGly 100
Db 241 GCTGCTGCAAGCGGTGTGTGGCGGAGGCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 101 GlyAlaGlySerGlyGluGlyAlaArgSerLysProThrThrArgArgProLysProPro 120
Db 301 GCGCGGGGAGCGCGCGAGGCTGACGCGACAGCATATAGCGCGCGCGCGCGCGCGCGCGCG 360
QY 121 TyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyLysArgLeuThr 140
Db 361 TACTCGACATCGCGCTCATCGCATGCGCATGCGCGCATGCGCGCGCGCGCGCGCGCGCGCG 420
QY 141 LeuAlaGluIleAsnGlyTyrLeuMetGlyLysPheProPheAlaGlySerTyrThr 160
Db 421 CTGGCGGAGATCAACGAGTCACTCATGCGCAAGTTCCTTTTCCCGCGCGCGCGCGCGCG 480
QY 161 GlyThrArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeu 180
Db 481 GGTGGCGCAACTCGTCCGCGCACACCTTTCGCTCAACGACTGCTTCAGTAGTGTG 540
QY 181 ArgAspProSerArgProTyrpGlyLysAspAsnTyrTrrMetLeuAsnProAsnSerGlu 200
Db 541 CGGACCCCTCGGGGCTGGGGGCAAGACACTACTGATGCTCAACCCCAACAGAGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgLysArgLeuSerHisArgAlaPro 220
Db 601 TACACCTTCGCCGACGGGGTCTTCGCCGCGCGCGAGAGGCTTCAGCCACCGCGGGCGG 660
QY 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGCGCGCGCGCGCGAGGAGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCC 720
QY 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGluAlaArgAla 260
Db 721 GCGCGCGCGCGCGCGCGCGCTGCGCGCGCATGCGCTCGCGCGCGCGCGCGCGCGCGCC 780
QY 261 SerProAlaGlyLysPheSerSerSerPheAlaAlaAspSerIleLeuArgLysProPhe 280
Db 781 AGCCCGCGCGCGCAAGTTCTCCAGCTCTTCGCCATCGACAGCATCTGCGCAAGCCCTTC 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrrpGlyAlaAlaPro 300
Db 841 CGCAGCGCGTGCCTCAGGAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 900

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QY 301 CysProProleuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
 Db 901 TGCCCGCGCTGCCCGCTCCCGCTCCCGCGCGCTCCCGCGCGCTCCCGCGCGCTCCG 960
 QY 321 ProLeuCysAlaTyrGlyAlaGlyAlaProAlaArgLeuGlyAlaArgGlyAlaGlyVal 340
 Db 961 CCGCTGCGCGTACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
 QY 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaAlaPro 360
 Db 1021 CCACCGACCGCGCGCGCTCCCTGCACTCTCCCGCGCGCGCGCGCGCGCGCGCGCG 1080
 QY 361 LeuArgGlyProAlaAlaGlyAlaAlaHisLeuTyrCysProLeuAlaGlyLeuProAla 380
 Db 1081 CTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
 QY 381 LeuGlnAlaAlaLeuValaArgArgProGlyProHisLeuSerTyrProValaGlyThrLeu 400
 Db 1141 CTCGAGCGCGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
 QY 401 LeuAla 402
 Db 1201 CTAGCT 1206

RESULT 5

US-10-650-112-25
 ; Sequence 25, Application US/10650112
 ; Publication No. US20040110712A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARKOWITZ, Sanford D.
 ; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
 ; FILE REFERENCE: CWRU-P01-044
 ; CURRENT APPLICATION NUMBER: US/10/650,112
 ; CURRENT FILING DATE: 2003-08-26
 ; PRIOR APPLICATION NUMBER: 10/274,177
 ; PRIOR FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: 10/229,245
 ; PRIOR FILING DATE: 2002-08-26
 ; PRIOR APPLICATION NUMBER: 60/406,296
 ; PRIOR FILING DATE: 2002-08-27
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patent version 3.2
 ; SEQ ID NO 25
 ; LENGTH: 1212
 ; TYPE: DNA
 ; ORGANISM: HUMAN FOXQ1
 US-10-650-112-25

Alignment Scores:

Pred. No.: 1,54e-291 Length: 1212
 Score: 324.00 Matches: 324
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 80.60% Indels: 0
 DB: 17 Gaps: 0

US-10-087-080-32 (1-402) x US-10-650-112-25 (1-1212)

QY 61 GlyAspGlyGluGlnSerAlaGlyGlyGlyProGlyAlaGluGluAlaLeuProAlaAla 80
 Db 184 GGCAGCGCGCAACAGAGTGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 243
 QY 81 AlaAlaAlaAlaValAlaAlaGluGlyAlaGluAlaGlyAlaAlaGlyProGlyAlaGly 100
 Db 244 GCTCTGAGCGGAGTGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 303
 QY 101 GlyAlaGlySerGlyGluGlyAlaAlaArgSerTyrThrArgArgProGlyProPro 120
 Db 304 GCGCGCGGAGCGGAGGAGTGGCGAGCGCGCAAGCACTTACGCGCGCGCGCGCGCGCG 363
 QY 121 TyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyAlaArgLeuThr 140
 Db 364 TACTCGTACATCGGCTCATCGCCATCGCCGACCTGCGCGCGCGCGCGCGCGCTTGACG 423

QY 141 LeuAlaGlyIleLeuGlyTyrLeuMetGlyGlyPheProPheAlaGlySerTyrThr 160
 Db 424 CTGGCGAGATTCACGAGTACCTCATGGGAGAGTTCCTCTTTTCCCGGAGCTACACG 483
 QY 161 GlyTyrArgAsnSerValaGlnHisAsnLeuSerLeuAsnAspCysPheValaValLeu 180
 Db 484 GGTGGCGCAACTCCGAGGCCACACCTTTCCTCAACAGACTGCTTGTAAAGTCTG 543
 QY 181 ArgAspProSerArgProTyrGlyAspAsnTyrTrpMetLeuAsnProAsnSerGlu 200
 Db 544 CGGACCCCTCGCGCGCTCGGCGCAAGGACCACTACGATGCTCAACCCACAGCGAG 603
 QY 201 TyrThrPheAlaAspGlyValaPheAlaArgArgAlaGlyLeuSerHisArgAlaPro 220
 Db 604 TACACCTTCGCGAGCGGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 663
 QY 221 ValProAlaProGlyLeuArgProGlyGluAlaProGlyLeuProAlaAlaProProPro 240
 Db 664 GTCCCGCGCGCGCGCTGCGCGCGCGAGAGCGCGCGCGCTCCCGCGCGCGCGCGCG 723
 QY 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGluArgAla 260
 Db 724 GCGCGCGCGCGCGCGCGCTCGCGCGCATGCGCTCGCGCGCGCGCGCGCGCGCGCG 783
 QY 261 SerProAlaGlyGlyPheSerSerPheAlaIleAspSerIleLeuArgGlyProPhe 280
 Db 784 AGCCCGCGGAGAGTTCACAGCTCTTCGCGCATGACAGCATCTCGCGCAAGCCCTTC 843
 QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlyThrGlyAlaAlaPro 300
 Db 844 CCGAGCGCGCGCTACAGGACACGCGCGCGGACACCTTCAGTGGAGCGCGCGCGCG 903
 QY 301 CysProProleuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
 Db 904 TGCCCGCGCTGCCCGCTCCCGCGCTCCCGCGCGCTCCCGCGCGCGCGCGCGCGCG 963
 QY 321 ProLeuCysAlaTyrGlyAlaGlyAlaProAlaArgLeuGlyAlaArgGlyAlaGlyVal 340
 Db 964 CCGCTGCGCGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1023
 QY 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaAlaPro 360
 Db 1024 CCACCGACCGCGCGCGCTCCCTGCTTGCATCTTCGCGCGCGCGCGCGCGCGCGCGCA 1083
 QY 361 LeuArgGlyProAlaAlaGlyAlaAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380
 Db 1084 CTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1143
 QY 381 LeuGlnAlaAla 384
 Db 1144 CTGACGCGCGCG 1155

RESULT 6

US-10-650-112-26
 ; Sequence 26, Application US/10650112
 ; Publication No. US20040110712A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARKOWITZ, Sanford D.
 ; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
 ; FILE REFERENCE: CWRU-P01-044
 ; CURRENT APPLICATION NUMBER: US/10/650,112
 ; CURRENT FILING DATE: 2003-08-26
 ; PRIOR APPLICATION NUMBER: 10/274,177
 ; PRIOR FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: 10/229,245
 ; PRIOR FILING DATE: 2002-08-26
 ; PRIOR APPLICATION NUMBER: 60/406,296
 ; PRIOR FILING DATE: 2002-08-27
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patent version 3.2
 ; SEQ ID NO 26
 ; LENGTH: 1203

	TYPE: DNA	
	ORGANISM: MOUSE FOXQ1	
	US-10-650-112-26	
	Alignment Scores:	
Pred. No.:	2.83e-96	Length: 1203
Score:	114.00	Matches: 114
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	28.36%	Indels: 0
DB:	17	Gaps: 0
US-10-087-080-32 (1-402) x US-10-650-112-26 (1-1203)		
OY	105 GtGtGtGtAlAAGSerSeryProTyrThrArgAProLYsProProTySerTyrIle	124
Dd	304 GGCGAGGGCGCGCGCAGAAGCCGTACACGCCGGGCCCAACCCTCATCTTCATCATC	363
OY	125 AlAleutLealAmelaailEArGasPseralaglglYargLeuThreuaLagluile	144
Dd	364 GCTCATATCGCATATGGCCATCCGCACACTCCGGGGGAGCAGCCTGTGAACAATGCCAGATC	423
OY	145 AsnglutyrlEueMeGLyLSFheProPhePheAgGLySetTyrThrGlYTrpArgan	164
Dd	424 AACGAGTACCTCATGGGAGCAAGTTCCCTTTTCCGGGGGAGGTACACGGGGCTGGCGAAC	483
OY	165 SerValaaghIsasrLeuSerLeuasnAspCySPhevallySeValleuArgAspprosEr	184
Dd	484 TCCGGCGCCACAAACCTTCGCTCAACGACTGTTCGTAAAGTGCTGGCGACCCCTCG	543
OY	185 ArgProTPrgLYLASpasantYrrTpMeLleuAsnProAsnserglutYrThrPheala	204
Dd	544 CGGCCCTGGGGAGGACAACTACTGTGATGCTCAACCCCAACGCAATACACTTCGGCC	603
OY	205 AspGlyValPheaRgARgARgARgLyASrLeuSerHisArg	218
Dd	604 GAAGGGGTCTTCGGCGCGCGCGCAAGCGCCTCACGACACCGG	645
	RESULT 7	
	US-10-650-112-27	
	; Sequence 27, Application US/10650112	
	; Publication No. US20040110712A1	
	GENERAL INFORMATION:	
	APPLICANT: MARKOWITZ, Sanford D.	
	TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS	
	FILE REFERENCE: CMRU-P01-044	
	CURRENT APPLICATION NUMBER: US/10/650,112	
	CURRENT FILING DATE: 2003-08-26	
	PRIOR APPLICATION NUMBER: 10/274,177	
	PRIOR FILING DATE: 2002-10-18	
	PRIOR APPLICATION NUMBER: 10/229,245	
	PRIOR FILING DATE: 2002-08-26	
	PRIOR APPLICATION NUMBER: 60/406,296	
	PRIOR FILING DATE: 2002-08-27	
	NUMBER OF SEQ ID NOS: 27	
	SOFTWARE: PatentIn version 3.2	
	SEQ ID NO 27	
	LENGTH: 1203	
	TYPE: DNA	
	ORGANISM: RAT FOXQ1	
	US-10-650-112-27	
	Alignment Scores:	
Pred. No.:	2.83e-96	Length: 1203
Score:	114.00	Matches: 114
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	28.36%	Indels: 0
DB:	17	Gaps: 0
US-10-087-080-32 (1-402) x US-10-650-112-27 (1-1203)		
OY	105 GtGtGtGtAlAAGSerSeryProTyrThrArgAProLYsProProTySerTyrIle	124

Db	304	GGTAGGAGCGCGGCGAGAACCGCTTACACGCGGCGGCCAACGCCCTTACTCTACATC	363
QY	125	AlaLeuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThrLeuAlaGluIle	144
Db	364	GCATCTATTCGCATCGGCATCTCGCGACTCCGCGGCGGAGACCTGACGCTGCGCCAGATC	423
QY	145	AsnGluIyrIleuMetGlyIysPhePheProPheArgGlySerIyrThrGlyTyrArgAsn	164
Db	424	AACAGATACCTCAAGGGGCAAGTCTCCCTTTTTCGGGGGAGCTTACACGGGCTGGCGCAAC	483
QY	165	SerValArgHisAsnLeuSerIleuAsnAspCysPheValIysValIleuArgAspProSer	184
Db	484	TCCGTGCGCCACCAACTCTCGCTCACAGACTGTTCGTCAAGGTCTGGCGACCCCTCG	543
QY	185	ArgProTIpGlyIysAspAsnIyrTyrMetIleuAsnProAsnSerGluTyrThrPheAla	204
Db	544	CGGCGCTGGGCAAGAGCAATTACTGATGTCTCAACCCCAAGGAAATACACTTCCTGCC	603
QY	205	AspGlyValPheArgArgArgArgIysArgIeuSerHisArg	218
Db	604	GACGGGAGTCTTCGCGCGCGCGCAAGGAGCTTCAGCCACCGG	645

RESULT 8

US-10-152-319A-1814

/ Sequence 1814, Application US/10152319A

/ Publication No. US20040072160A1

/ GENERAL INFORMATION:

/ APPLICANT: Mendrick, Donna

/ APPLICANT: Porter, Mark

/ APPLICANT: Johnson, Kory

/ APPLICANT: Higgs, Brandon

/ APPLICANT: Castle, Arthur

/ APPLICANT: Elashoff, Michael

/ TITLE OF INVENTION: Molecular Toxicology Modeling

/ FILE REFERENCE: 44921-5089-US

/ CURRENT APPLICATION NUMBER: US/10/152,319A

/ CURRENT FILING DATE: 2002-05-22

/ PRIOR APPLICATION NUMBER: US 60/292,335

/ PRIOR FILING DATE: 2001-05-22

/ PRIOR APPLICATION NUMBER: US 60/297,523

/ PRIOR FILING DATE: 2001-06-13

/ PRIOR APPLICATION NUMBER: US 60/298,925

/ PRIOR FILING DATE: 2001-06-19

/ PRIOR APPLICATION NUMBER: US 60/303,810

/ PRIOR FILING DATE: 2001-07-10

/ PRIOR APPLICATION NUMBER: US 60/303,807

/ PRIOR FILING DATE: 2001-07-10

/ PRIOR APPLICATION NUMBER: US 60/303,808

/ PRIOR FILING DATE: 2001-07-10

/ PRIOR APPLICATION NUMBER: US 60/315,047

/ PRIOR FILING DATE: 2001-08-28

/ PRIOR APPLICATION NUMBER: US 60/324,928

/ PRIOR FILING DATE: 2001-09-27

/ PRIOR APPLICATION NUMBER: US 60/330,867

/ PRIOR FILING DATE: 2001-11-01

/ PRIOR APPLICATION NUMBER: US 60/330,462

/ PRIOR FILING DATE: 2001-10-22

/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 2221

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 1814

/ LENGTH: 1760

/ TYPE: DNA

/ ORGANISM: Rattus norvegicus

/ FEATURE:

/ OTHER INFORMATION: Genbank Accession No. NM_022858

US-10-152-319A-1814

Alignment Scores:

Prod. No.: 3.9e-96 Length: 1760

Score: 114.00 Matches: 114

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.36% Indels: 0
DB: 12 Gaps: 0
US-10-087-080-32 (1-402) x US-10-152-319A-1814 (1-1760)

QY 105 GlyGluGlyAlaArgSerLeuProThrArgProLeuProProTyrSerTyrIle 124
Db 508 GGTAGAGGCGCGCCAGCAAGCCCTTACAGCGGCGCCCAAGCCCTTCTCTACATC 567
QY 125 AlaLeuIleAlaMetAlaIleArgAspSerAlaGlyAlaArgLeuThrLeuAlaGluIle 144
Db 568 GCATCTATCCGCAATGAGCATCCGCGGCGGAGCGCTGACGCTGCGCGAATC 627
QY 145 AsnGluThrLeuMetGlyLysPheProPheArgGlySerTyrThrGlyTyrArgAsn 164
Db 628 AACGAGTACTCATGGGCAAGTTCCTTTTCGCGGCGAGCTACACAGGCGCTGCGGAC 687
QY 165 SerValArgHisAsnSerLeuAsnAspCysPheValLysValLeuAlaGlyProSer 184
Db 688 TCGGTGGCCACAACTCTGCTCAACGACTGTTGTCAGGTGCTGCGCGACCTCG 747
QY 185 ArgProTyrGlyLysAspAsnTyrTrpMetLeuAsnProAsnSerGluTyrThrPheAla 204
Db 748 CGGCGCTGGGGCAAGACATTACTGATGCTCAACCCCAACGCAATACCTTGCC 807
QY 205 AspGlyValPheArgTrgArgGlyAlaGluSerHisArg 218
Db 808 GACGGGGGTCTTCGCGCGCGCGCAAGCGCTCAGCACCGG 849

RESULT 9
US-10-027-632-231353/c
; Sequence 231353, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231353
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231353

Alignment Scores:
Pred. No.: 2.06e-58 Length: 585
Score: 73.00 Matches: 120
Percent Similarity: 98.36% Conservative: 0
Best Local Similarity: 98.36% Mismatches: 1
Query Match: 18.16% Indels: 2
DB: 13 Gaps: 0
US-10-087-080-32 (1-402) x US-10-027-632-231353 (1-585)

QY 264 GlyLysPheSerSerPheAlaIleAspSerIleuArgLysPProPheArgSerArg 283
Db 583 GGCAAGTCTCCAGCTCTCTGCGCATGACAGATCTCTGCGCAAGCCCTTCGCGAGCGC 524
QY 284 ArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrpGlyAlaAlaProCysProPro 303
Db 523 CGCTCAGGAGACAGGCGCCCGGAGAGAGCTTCAAGTGGGGCGCGCCCTGCGCCGCG 464
QY 304 LeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeuProLeuCys 323
Db 463 CTGCGCGGTTCCTCCGCGCTCTCCCGCGCGCCCTGCGAGGGCGCTGCGCTGCG 404
QY 324 AlaTyrGlyAlaGlyLysPProAlaArgLeuGlyAlaArgGluAlaGluValProProth 343
Db 403 GCGTACGGCGCGGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 345
QY 343 rAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysProLeuArgG1 363
Db 344 CGCGCGCGCGCTCTGCTGACCTCTCCCGGCGGCGCGCGCGCGCGCGCGCGCGCG 285
QY 363 yProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAlaLeuGlnAl 383
Db 284 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 225
QY 383 aAla 384
Db 224 GGCC 221

RESULT 10
US-10-027-632-231353/c
; Sequence 231353, Application US/10027632
; Publication No. US2003024075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231353
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231353

Alignment Scores:
Pred. No.: 2.06e-58 Length: 585
Score: 73.00 Matches: 120
Percent Similarity: 98.36% Conservative: 0
Best Local Similarity: 98.36% Mismatches: 1
Query Match: 18.16% Indels: 2
DB: 16 Gaps: 0
US-10-087-080-32 (1-402) x US-10-027-632-231353 (1-585)

QY 264 GlyLysPheSerSerPheAlaIleAspSerIleuArgLysPProPheArgSerArg 283
|||||

Db 583 GGCAAGTTCTCCAGCTCTTGCATCGACAGCATCTCGGCAAGCCCTTCGGCAGCCG 524
QY 284 ArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrpGlyAlaAlaProCysProPro 303
Db 523 CCCCTTCAGGAGACACGGCCCGGAGAGAGCTTCACTGGGGGCGCGCGCTCGCCGCGCG 464
QY 304 LeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeuProCys 323
Db 463 CTGCCCGCGCTCCCGCGCTCTCCCGCGCGCGCTCGAGGCGCTGCTGCGCGCTCTGC 404
QY 324 AlaTyrGlyAlaGlyGlnProAlaArgGlyAlaArgGlnAlaGlyAlaProProth 343
Db 403 GGTACGGGGCGGGCGAGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGAGC 345
QY 343 rAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysProLeuArg 363
Db 344 CGGGCGCGCGCTCTCTCTTGCACCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGAG 285
QY 363 yProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAlaLeuGlnAl 383
Db 284 CCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGC 225
QY 383 aAla 384
Db 224 GGCC 221

RESULT 11

US-09-833-381-1266
; Sequence 1266, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/516,448
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1266
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(320)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1266

Alignment Scores:

Pred. No.: 1.65e-20 Length: 320
Score: 32.00 Matches: 45
Percent Similarity: 97.83% Conservative: 0
Best Local Similarity: 97.83% Mismatches: 0
Query Match: 7.96% Indels: 1
DB: 9 Gaps: 0

US-10-087-080-32 (1-402) x US-09-833-381-1266 (1-320)

QY 220 ProValProAlaProGlyLeuArgProGlnGlnAlaProGlyLeuProAlaAlaProPro 239
Db 92 CCGGTCGCCCGCGCGCGCTCGGCGCGAGGAGCGCGCGGCTCTCCCGCGCGCGCGCGCN 151
QY 240 Pro-AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGlnGln 259
Db 152 CTTCCGCGCGCGCGCGCGCGCTCGCGCGCATGCGCTGCGCGCGCGCGCGAGAGAGCG 211
QY 259 gAlaSerProAlaGly 264
Db 212 CGCCAGCGCGCGCGCGCG 227

RESULT 12

US-09-918-995-4735
; Sequence 4735, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4735
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(477)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4735

Alignment Scores:

Pred. No.: 0.00126 Length: 477
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 10 Gaps: 0

US-10-087-080-32 (1-402) x US-09-918-995-4735 (1-477)

QY 118 LysProProTyrSerTyrIleAlaLeuIleAlaMetAlaIle 131
Db 105 AAGCTCCCTACAGCTACATCGCCCTTATGCTATGGCCATC 146

RESULT 13

US-09-908-975-24908
; Sequence 24908, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Iliat
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 3668-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24908
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-24908

Alignment Scores:

Pred. No.: 0.0172 Length: 65
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.99% Indels: 0
DB: 10 Gaps: 0

US-09-908-975-24908

QY 118 LysProProTyrSerTyrIleAlaLeuIleAlaMetAlaIle 131
Db 105 AAGCTCCCTACAGCTACATCGCCCTTATGCTATGGCCATC 146

US-10-087-080-32 (1-402) x US-09-908-975-24908 (1-65)
Qy 391 ProHisLeuSerLeuAsnGlyThrLeuValys 402
Db 3 CGGCACCTGCTCTACCGGTGAGACCTGCTGACT 38
RESULT 14
US-10-029-386-23708
; Sequence 23708, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: A60MICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ. ID NOS: 2001-12-20
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ. ID NO 23708
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR2.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
; OTHER INFORMATION: SWISSPROT HIT: Q60688, EVALUATE 1.00e-58
; OTHER INFORMATION: EST HUMAN HIT: AM236501.1, EVALUATE 3.00e-76
; OTHER INFORMATION: NT HIT: U13223.1, EVALUATE 0.00e+00
US-10-029-386-23708
Alignment Scores:
Pred. No.: 0.0639 Length: 312
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.99% Indels: 0
DB: 15 Gaps: 0
US-10-087-080-32 (1-402) x US-10-029-386-23708 (1-312)
Qy 167 ArgHisAsnLeuSerLeuAsnGlyThrLeuValys 178
Db 158 CGGCACCAACCTCTCGCTGACGACCTGCTGCAAG 193
RESULT 15
US-10-027-632-138699
; Sequence 138699, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,356

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ. ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 138699
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-138699
Alignment Scores:
Pred. No.: 0.0829 Length: 425
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.99% Indels: 0
DB: 13 Gaps: 0
US-10-087-080-32 (1-402) x US-10-027-632-138699 (1-425)
Qy 167 ArgHisAsnLeuSerLeuAsnGlyThrLeuValys 178
Db 238 CGGCACCAACCTCTCGCTGACGACCTGCTGCAAG 273
Search completed: September 2, 2004, 19:43:22
Job time : 605 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 2, 2004, 15:09:29 ; Search time 96 Seconds

(without alignments)
2323.857 Million cell updates/sec

Title: US-10-087-080-32
2123
Perfect score: 1 MKLEVFYPRRAHGDKQSD.....AALVRPPLHLYSVETLLA 402
Sequence:

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 segs, 27747546 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:
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-DB=Issued Patents NA -QPM=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOFCU=0
-LIST=45 -DOCALLIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10087080@cgn1.1.56@runat.27082004.104031.13248 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Issued Patents NA:*
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3: /cg2_6/prodata/2/ina/6A.COMB.seq:*
4: /cg2_6/prodata/2/ina/6B.COMB.seq:*
5: /cg2_6/prodata/2/ina/6C.COMB.seq:*
6: /cg2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	22.1	320	US-09-833-381-1266	Sequence 1266, Ap
2	468.5	22.1	3946	US-09-083-351-1	Sequence 1, Appli
3	468.5	22.1	3946	US-09-083-352-1	Sequence 1, Appli
4	446.5	21.0	1965	US-09-220-132-21	Sequence 21, Appli
5	425	20.0	1659	US-09-083-351-3	Sequence 3, Appli
6	425	20.0	1659	US-09-083-352-3	Sequence 3, Appli
7	404.5	19.1	1860	US-08-331-644-3	Sequence 3, Appli
8	404.5	19.1	1860	US-08-331-644-3	Sequence 3, Appli
9	403.5	19.0	1309	US-09-976-594-927	Sequence 927, App
10	400.5	18.9	2830	US-07-882-292-1	Sequence 1, Appli
11	400.5	18.9	2830	US-08-331-644-1	Sequence 1, Appli
12	400.5	18.9	2830	US-08-331-644-1	Sequence 1, Appli

13	360.5	17.0	1155	US-08-331-644-4	Sequence 4, Appli
14	360.5	17.0	1155	PCT-US93-04102-4	Sequence 4, Appli
15	324.5	15.3	5080	US-09-976-594-495	Sequence 495, App
16	309.5	14.6	1605	US-09-087-134-10	Sequence 10, Appli
17	307	14.5	1634	US-09-087-134-13	Sequence 13, Appli
18	306.5	14.4	1793	US-09-113-309-1	Sequence 1, Appli
19	306.5	14.4	1793	US-09-521-107A-1	Sequence 1, Appli
20	306.5	14.4	1793	US-09-521-107A-1	Sequence 1, Appli
21	297	14.0	1668	US-09-652-332-1	Sequence 1, Appli
22	264	12.4	2517	US-07-906-930E-1	Sequence 1, Appli
23	264	12.4	3465	US-09-023-655-1136	Sequence 1, Appli
24	263	12.4	2939	US-07-906-930E-3	Sequence 3, Appli
25	251.5	11.8	3394	US-09-620-312D-314	Sequence 3, Appli
26	236	11.1	3342	US-08-742-753-3	Sequence 3, Appli
27	233.5	11.0	3441	US-08-742-753-3	Sequence 3, Appli
28	231	10.9	4411529	US-09-103-840A-1	Sequence 1, Appli
29	229.5	10.8	4403765	US-09-103-840A-2	Sequence 1, Appli
30	228.5	10.8	2888	US-08-765-507A-1	Sequence 2, Appli
31	226	10.6	4411529	US-09-103-840A-1	Sequence 1, Appli
32	224	10.6	4403765	US-09-103-840A-2	Sequence 1, Appli
33	216	10.2	1869	US-09-372-668-3	Sequence 2, Appli
34	216	10.2	1869	US-09-697-377-3	Sequence 3, Appli
35	216	10.2	1869	US-09-696-868-3	Sequence 3, Appli
36	216	10.2	1869	US-09-697-341-3	Sequence 3, Appli
37	211.5	10.0	12001	US-08-458-568A-11	Sequence 11, Appli
38	210.5	9.9	2481	US-09-894-998A-35	Sequence 35, Appli
39	210.5	9.9	12425	US-09-616-289-50	Sequence 50, Appli
40	208	9.8	8438	US-07-945-283-1	Sequence 1, Appli
41	207.5	9.8	2150	US-08-318-837-1	Sequence 1, Appli
42	206.5	9.7	2561	US-09-616-289-48	Sequence 48, Appli
43	205.5	9.7	2109	US-09-370-838-153	Sequence 153, App
44	204	9.6	34094	US-09-292-034-1	Sequence 1, Appli
45	203	9.6	12001	US-08-458-568A-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-833-381-1266
Sequence 1266, Application US/09833381
Patent No. 6672186
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1266
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(320)
OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1266

Alignment Scores:

Pred. No.: 1.09e-17 Length: 320
Score: 470.00 Matches: 94
Percent Similarity: 89.62% Conservative: 1
Best Local Similarity: 88.68% Mismatch: 9
Query Match: 22.14% Indels: 2
DB: 4 Gaps: 0

US-10-087-080-32 (1-402) x US-09-833-381-1266 (1-320)

Qy 190 AspsanTYTTPmctLeuasnProasSercJutYrThrPhealAaapGLVvalPhearg 209

Db	2	GACAACTACTGGATGTCTAAACCCAAAGCAGGTACACTTTCGCCGAGGGAGCTTCGCG	61
QY	210	ArgAArgLYsArgLeuSerHisArgAlaProValProAlaProGlyLeuArgProGlu	225
Db	62	CGCGCGCGCAAGGCGCTCAACCAACGCMGCGCGGTCCCGCGCCGGAGCTCGGCGCGAG	121
QY	230	GluAlaProGlyLeuProAlaAlaProProProAlaProAlaAlaProAlaSerProAr	245
Db	122	GAGGCCCGGGGCTCCCGCGCGCGCCGCGCCCTCCGCGCGCGCGCGCTCGCGCGG	181
QY	249	GMeArArgSerProAlaAlaArgGluGluArgAlaSerProAlaGlyLysPheSerSerSe	265
Db	182	CATGCGCTGCGCCGCGCGCGCAAGAAAGCGCGCCAGCCCGCGGGGCAANTTCTCCANTC	241
QY	269	rPheAlaIleAspSerIleLeuArgLysProPheArgSerArgGlyLeuArgAspThrA	285
Db	242	CTTCNATCATCTCAAGACATCTGCNCAATCCCTTCGCAATCGCGCGCTCANAGACACGG	301
QY	289	IaProGlyThrThr	293
Db	302	CCCCCGGAGACACC	315

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Score:	468.50	Matches:	155
Percent Similarity:	38.92%	Conservative:	44
Best Local Similarity:	30.73%	Mismatches:	14
Query Match:	22.07%	Indels:	18
DB:	3	Gaps:	23

US-10-087-080-32 (1-402) X US-09-083-351-1 (1-3946)

QY	8	ProAlaGAlaAlaHisIaGlyAspIySGInGlySerAspIeuGIuGIaIaGlyIySerAsp	27
Db	287	CCGAGGGCGCCGAGAGCCAGCCACCAGCGAGCGCGGAGAGGGCGAGCGAGCCGAGC	346
QY	28	Ala-----ProSerProIeuSerAlaIaGlyAspAspSerIeuGlySerAsp	43
Db	347	GCAAGCGCAGCGAGGGGCGCGAGCACA---GCTGGCGCGGGCCCGGACTCGGACTCGCGCGCC	403
QY	44	GlyAspCysAlaAlaIaIyAspSerAlaGlyIyGlyIaIaIaGAspThrGIuGlyAspGly	63
Db	404	GAGCGCGGCGCGCCCGCGCCGAGCGAGGGGTGGGGGGCGCGCGCGCGCGGGGGCGCGCGC	463
QY	64	GIuGInSerAlaGlyIyGlyIyProGlyYAlaGIuGIuAlaIaIeProAlaAlaAla-----	81
Db	464	GAGCGG-----GGGCGCA---TGCGAGCGCGCTACTCCGTGTCAGCCCGCAACT	508
QY	82	-----AlaAlaAlaValValAlaIaGlyIyAlaGIuAlaGly	93
Db	509	CCCTGGAGTGGTGGCTTACCTCGGCGCGAGAGACTACTACCGC--GCGCGCGCGCG	567
QY	94	AlaAlaGlyProGly-----	98
Db	568	GGCGCGGGGGGGCGCTTACACCGCGCATGCGGGCCCCCATGAGCGTACTCGCACCTCGCG	627
QY	99	-----AlaGlyIyIaGlySerGIyGIuGIyAlaIaGlySerIySProTyr	113
Db	628	CACGCCGAGAGTACCOCGGGGCGCATGGCGCGCGCTGACGG-----CCCTAC	675
QY	114	ThrArgArgPro-----LysProProTyrSerTyrIleAlaIeuIle	127
Db	676	ACGCGCGACCCCGACGCCAGAGCATGGTGAAAGCGCCCTTAAGTACATCGCGCTTATC	735
QY	128	AlaMetAlaIleArgAspSerAlaGlyIyArgIeuThrIeuAlaGluIleAsnGIuTyr	147
Db	736	ACCATGGCATCAGAAAGCGCCCGGACAAAGAAAGATCACTTAACGGCATCTTACCAAGTTTC	795
QY	148	LeuMetGlyIyAspPheProPhePheArgIySerTyrThrGIyTPRArgAsnSerValArg	167
Db	796	ATATATGACCGCTCTCCCTTTCATCCGGGACAAACAGACAGGCTGGGAGAAACAGATCCGC	855
QY	168	HisAsnIeuSerIeuAsnAspCysPheValIyValIeuIaArgAspProSerArgProTyr	187
Db	856	CACAACTCTCGCTCAACGATGCTTCGTCAAGTGTCCGCGGACACAAAGAAAGCG---	912
QY	188	GlyIyAspAsnTyrThrMetIeuAsnProAsnSerGIuTyrThrPheAlaAspGIyAla	207
Db	913	GGCAAGGGCAGCTACTGAGCGCTGGACCCGGACTCTTACAACATGTTTCGAAGAAAGGCGAGC	972
QY	208	PheArgArgArgIyArgIyLeuSerHis-----	217
Db	973	TTCCTGGGGCGGGCGGGCGCTTCAGAAAGAAAGACGGGTGAAGAGCAAGAGGAAG	1033
QY	218	-----ArgAlaProAlaProAlaProGly	225
Db	1033	GACAGCGTGACCTCAAGAGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	108
QY	226	LeuArgProGIuGIuAlaProGlyIleuProAlaAlaPro-----	238
Db	1090	-----CCGAGAGCAGGGCGAAGGAGCGCGCGGTCCGAGCGCGCGCGCGCGCGCATC	1144
QY	239	-----ProProAlaProAlaAlaProAla	246
Db	1144	CAGAGATCAAGACCGAAGACGATACGTGCCCTCGCGCGCGCGCGCGCGCGCGCGCG	1220
QY	247	Ser-----ProArgMetArgSerPro-----	253

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Db 1204 GCCGCCCTGGGAGGAGGAGGCGCGCGGTGCTCCAGATCGAGAGCCCGGAGAGAGC 1263
QY 254 ---AlaArgIngluArgAlaSerProAlaGlyysPhe----- 266
Db 1264 AGCAGCAGCCTGTCAGGAGGAGAGAGCCCGGAGAGCTGCGCTGCGCGCGCGCTC 1333
QY 266 ----- 266
Db 1324 AGCTGAGCGTGGGATTCCGCGCGCGCGCGCGCGCTCGCGCGCGCGCGAGC 1393
QY 267 ---SerSerSerPheAlaAlaSerSerIleuArglys----- 278
Db 1384 CATAGCAGGCTTCAGCGTGCATGACATGACGTCGCGCGGAGTCCGCGAGAGC 1443
QY 279 -----ProPheArgSerArgArgLeuArgAspThrAlaProG 1503
Db 1444 GCGGCGCGGAGCTGAGCTCCGCGCTTCTGCGCTCGCGCGCGCGCTCGCGCGG 1503
QY 291 YThrThrLeuGlnTrpGlyAlaAlaProCysProProLeuProAlaPheProAlaLeu 311
Db 1504 ATGCGACCCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1563
QY 311 UPProAlaAla-----ProCysArgAlaLeuLeuProLeuCysAlaTrpGlyAlaGly 329
Db 1564 CCGTGGAGCCAGACTTCAGCGCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCG 1623
QY 329 UPProAlaArgLeuGlyAlaArgGluAlaGluValProProThrAla-----ProPr 346
Db 1624 G-----CGGGGGCGCGCGCGCGCGCGCGCGCGAGCTTGCACACTGCAAGCCATG 1674
QY 346 GLeuLeuLeuAlaProLeu-----ProAlaAlaAlaPr 357
Db 1675 AGCCTGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1734
QY 357 GAlaArgProLeuAlaArgGlyProAlaAlaGlyAlaHisLeuTrpCysPro----- 374
Db 1735 GGGTCCGCGCGTGCAGCAACCCCG-----TGCCCGACTACTCT 1770
QY 375 ---LeuArgLeuProAlaAlaLeuGlnAlaAlaLeuValArgArgPro 389
Db 1771 CTCGCTCCGCTCACAGCAGCA-----GCTCGTGTCTCC 1804

RESULT 3
US-09-083-352-1
; Sequence 1, Application US/09083352
; Patent No. 6207450
; GENERAL INFORMATION:
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Stone, Edwin M.
; APPLICANT: Nishimura, Daryl J
; APPLICANT: Patel, Shiva
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,352
; FILING DATE: 22-MAY-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

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; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-029,01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3946 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 475..2133
; US-09-083-352-1

Alignment Scores:
Pred. No.: 1,87e-16 Length: 3946
Score: 468.50 Matches: 165
Percent Similarity: 38.92% Conservative: 44
Best Local Similarity: 30.73% Mismatches: 143
Query Match: 22.07% Indels: 186
DB: Gaps: 23

US-10-087-080-32 (1-402) X US-09-083-352-1 (1-3946)
QY 8 ProArgAlaAlaHisGlyAspLysGlnGlySerAspLeuGluGlyAlaGlySerAsp 27
Db 287 CCGAGGCGCGGAGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 346
QY 28 Ala-----ProSerProLeuSerAlaAlaGlyAspAspSerLeuGlySerAsp 43
Db 347 GCACAGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 403
QY 44 GlyAspCysAlaAlaAlaLysProSerAlaGlyGlyAlaAlaArgAspThrGlnGlyAspGly 63
Db 404 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463
QY 64 GluGlnSerAlaGlyGlyGlyProGlyAlaGluGluAlaAlaProAlaAlaAla----- 81
Db 464 GAGCGG-----GGGCGCA---TGAGGCGCGCTACTCTCGTGTCCAGCCCAACT 508
QY 82 -----AlaAlaAlaValAlaAlaGluGlyAlaGluAlaGly 93
Db 509 CCCTGGAGTGTGTGCCCTACTCTCGCGCGCGAGCAGACTACTACCGC-GCGGCGCGCG 567
QY 94 AlaAlaGlyProGly----- 98
Db 568 GCGGCGCGGCGCGCTACACCGCCATGCCGCCATGAGCGTGTACTGCACTCTGCG 627
QY 99 -----AlaGlyGlyAlaGlySerGlyGluGlyAlaAlaArgSerLysProTrp 113
Db 628 CACGCGAGCAGACCGCGCGCGCATGCGCGCGCGCTACAGG-----CCCTAC 675
QY 114 ThrArgArgPro-----LysProProTrpSerTrpIleAlaLeu 127
Db 676 ACGCGCAGCCCGCAGCCCAAGACATGTGAAGCCGCTTATAGTACATCGCGCTCATC 735
QY 128 AlaMetAlaAlaArgAspSerAlaGlyArgGluThrLeuAlaGluIleAsnGluTrp 147
Db 736 ACCATGGCCATCAGAGCGCCCGGAGCAAGAAATACCTTGAACGGCATCTACAGTTTC 795
QY 148 LeuMetGlyLysPheProPhePheArgGlySerTrpGlyTrpArgAsnSerValArg 167
Db 796 ATCATGAGACCGCTCCCTTTCACCGGAGCAACAGAGGCTCGGAGAAAGCATCCGC 855
QY 168 HisAsnLeuSerLeuAsnAspCysPheValLysValLeuArgAspProSerArgProTrp 187
Db 856 CACAACCTCTCGCTCAACAGGTCTTCGCAAGGTGCGCGCGAGCAAGAAAGCG--- 912
QY 188 GlyLysAspAsnTrpTrpMetLeuAsnProAsnSerGluTrpThrPheAlaAspGlyVal 207

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Db      913 GCGAAGGCGACGCTTCTGAGCGCTGAGACCCGACCTCTCAACAATGTTTCAGAAAGCGAGC 972
Qy      208 PheArgArgArgArgArgArgSerHis----- 217
Db      973 TTCTCGGGGGGGGGGGCGCTTCAAGAGAGAGACCGCGGTGAAGACAGAGAGAGAG 1032
Qy      218 -----ArgAlaProValProAlaProGly 225
Db      1033 GACAGGCTGACCTCAAGAGACCGCCCGCCGCGCCAGACCCCGCGCGCGCG-- 1089
Qy      226 LeuArgProGluGluAlaProGlyLeuProAlaAlaPro----- 238
Db      1090 -----CCGAGAGAGGGCCGAGCGCAAGCGCGCGCTCCGACGCGCGCGCGCGATC 1143
Qy      239 -----ProProAlaAlaProAlaAlaProAla 246
Db      1144 CAGGACATCAAGACCGAGAACGATAGTCCCTCGCGCGCCGACCCCTGTGCTCCCGGCC 1203
Qy      247 Ser-----ProArgMetArgSerPro----- 253
Db      1204 GCCCGCCCTGGGACGCGGACGCGCGCGCGGTGCTCCAGAGTCGAGAGCCCGACACAGC 1263
Qy      254 ---AlaArgGluGluGluArgAlaSerProAlaGlyLysPhe----- 266
Db      1264 AGCAGACGCTCTCCAGCGGAGAGACCCCGCGGACGCTGCGGTGCGCGCGCGCTC 1323
Qy      266 ----- 266
Db      1324 AGCCGTGAGCGGTGCGGATTCGCGCGCGCGCGCGCGCTCCGCGCCCGCGCGAC 1383
Qy      267 ---SerSerSerPheAlaAlaAspSerLeuLeuArgLys----- 278
Db      1384 CATAGCCAGGCGCTTCAGCGTGAACAACATCATGAGTGTGTCGCGGGGTGCGCCGACAGC 1443
Qy      279 -----ProPheArgSerArgArgLeuArgAspThrAlaProGly 291
Db      1444 GCGCGCGGAGACTCAGCTCCGCGCTTGTGCGCTGCGGCGCGCGCTCCTCGCGCGCGG 1503
Qy      291 YThrThrLeuGluThrGlyAlaAlaProCysProProLeuProAlaPheProAlaLeuLe 311
Db      1504 ATCGACACCCCGCTGCGCGCTGCGCTACTGCGCGCGACAGAGCTCCCTCTACAGCTCC 1563
Qy      311 uProAlaAlaAla-----ProCysArgAlaLeuLeuProLeuCysAlaTyArgAlaGly 329
Db      1564 CCTGCGACCCAGACCTCCAGCGCGGCGAGCTCGCGCGCGCGCGCGCGCGCGCGCC 1623
Qy      329 uProAlaArgLeuGlyAlaArgGluAlaGlyValProProThrAla-----ProPr 346
Db      1624 G-----CGGGGGGGCGCGCGCGCGCGCGGACCTTACACTGCAACCTGCAAGCCTG 1674
Qy      346 OleuLeuLeuAlaProLeu-----ProAlaAlaAlaPr 357
Db      1675 AGCTGTGACGCGCGCGGAGCGCGGCGCACTTGAAGGGCGCGCGCGCGCGCGCG 1734
Qy      357 AlaAlaArgProLeuArgGlyProAlaAlaGlyAlaHisLeuTyArgPro----- 374
Db      1735 GGTCTGGCGCGTGAACAACCCCG-----TGCCGCACTACTCT 1770
Qy      375 ---LeuArgLeuProAlaAlaLeuGluAlaAlaLeuValArgArgPro 389
Db      1771 CTGCTCGGCTGACCAAGAGCA-----GCTCGTCTGCTCC 1804

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; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-220-132-21

Alignment Scores:
Pred. No.: 1,31e-15 Length: 1965
Score: 446.50 Matches: 150
Percent Similarity: 44.55% Conservative: 42
Best Local Similarity: 34.80% Mismatches: 121
Query Match: 21.03% Indels: 120
DB: Gaps: 19

US-10-087-080-32 (1-402) x US-09-220-132-21 (1-1965)
Qy      28 AlaProSerProLeuSerAlaAlaGlyAspAspSerLeuGlySerAspGlyAspCysAla 47
Db      13 GCCCGAGAGACACACTCTCTCTCC-----TCGTGCTGCTCTCCGCTCTCTCGCGCC 63
Qy      48 AlaArgProSerAlaGlyGlyAlaArgAspThrGluArgSerGlyGluSerAla 67
Db      64 TCGCTCTGCTCTCTCTCTCAATTCGCGC----- 90
Qy      68 GlyGlyGlyProGlyAlaGluGluAlaAlaProAlaAlaAlaAlaValAla 87
Db      91 -----AGCGCCCTCTCGGTGCTGCAAG----- 114
Qy      88 GluGlyAlaGluAlaGlyAlaAlaGlyProGlyAlaGlyAlaGlySerGlyGlyGly 107
Db      115 -----AGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGGCGCGCC 156
Qy      108 AlaArgSerLysProTyThrArgArgPro---LysProProTyArgSerTyAlaAlaLeu 126
Db      157 AAGAGGCGAGCTCGGGGCTCGCGCGCGCGCGCGCGAGAGCCCTTACTGTAATCGCGCTC 216
Qy      127 IleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThrLeuAlaGluIleAsnGlu 146
Db      217 ATCGCATGCGCATTCAGACTCGGCCAGAGCGCGCTGACGCTCAAGAGATCTAACAG 276
Qy      147 TyrlauMetGlyLysPheProPhePheArgGlySerTyThrGlyTyArgAsnSerVal 166
Db      277 TTCTCGAGGCGCGCTTCTCTCTTCTCGCGCGCGCTTACCAAGGCTGGAAGAACTCGGTG 336
Qy      167 ArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeuArgAspProSerArgPro 186
Db      337 CGCACAACTCTCTCTCAAGAGAGCTTCTCAAGCTGCTCTAAGAGGCTCGGGGGCGCC 396
Qy      187 TrpGlyLysAspAsnTyTrpMetLeuAsnProAsnSerGlyTyThrPheAlaAspGly 206
Db      397 ---GCCAAGGGCGCACTAATGAGCACTGAGCCCGCGCAAGAGTCAATGTTGAGAGAGCGC 453
Qy      207 ValPheArgArgArgArgArgLeuSerHisArgAlaPro-----Val 221
Db      454 TCGTTCGCCCGCGCGCGC--GCGCGGCTTCAAGCGGAGAGTGCAGGCGCTCAAGCCATGTA 512
Qy      222 Pro-----AlaProGlyLeuArgPro 228
Db      513 CCACCGCGTGTGAGCGGCTTGGGCTTGGGGCGCTGCTGCTGCTCCCGAGGGCTTGA--- 569
Qy      229 GluGluAlaProGlyLeuProAlaAlaProProProAlaProAlaAlaProAlaSerPro 248
Db      570 -----CTTCCAGGCGCGCGCGCGCGCGCTCGGCTGCGTGCACAGCGAGG 614
Qy      249 ArgMetArgSerPro-----AlaArgGluGlu 257

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; US-09-220-132-21
; Sequence 21, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 0734-074001
; CURRENT APPLICATION NUMBER: US/09/220,132

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Qy      259 ArgAlaSerProAlaGlyTyrSph-----                266
Db      808 GGAAGACGACCCCGGGAGCCTGCCTGCGCGCGCGCGCTGACGTGACGTGACGTGACGT 867
Qy      267 -----                               SerSerSerPheAla 271
Db      866 TCCGCGCGCGCGCGCGCGCGCGCTTCGCCCGCGCGCGCACCATAGCAAGGCTTGAC 927
Qy      272 IleAspSerIleLeu-ArgLys-----                    278
Db      928 GTGACAACATCATGACGCTGCTGCGGGGCTGCCGAGAGCGCGCGCGAGCTGACG 987
Qy      279 ----ProPheArgSerArgArgIleuArgAspThrAlaProGlyThrThrLeuGlnTrpGl 297
Db      968 TTCGGCCCTTCGGCTCTGCGCGCGCGCGCTTCGCGCGCGGGGATGACACCCCGCTGCG 1047
Qy      297 YAlaAlaProCysProProLeuProAlaPheProAlaLeuLeuProAlaIla-----Pr 315
Db      1048 CTCGCGCGCTACTGCGCGCGCGCGAGAGCTCCCTCTACAGCTCCCCCTGAGGCTAAGACCTTC 1107
Qy      315 cCysArGAlaLeuLeuProLeuCysAlaTyrelYAlaGlyInuProAlaArgLeuGIYA1 335
Db      1108 AGCGCGGCGAGCTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG-----CGGGGGCGC 1158
Qy      335 aArgGluAlaGluValaProProThrAla-----ProProLeuLeuLeuAlaProLe 352
Db      1219 GAGCGCGGGGGCGCACTTGACAGGCGCGCGCGCGGGGGCGCGGGCGGCTGGAGAAC 1278
Qy      363 yProAlaAlaGlyGlyAlaHisLeuTyrcysPro-----LeuArgLeuProAl 379
Db      1279 CCCC-----TGCCCGACTACTCTGCGCTCGGCTACGACGAC 1314
Qy      379 aAlaLeuGlnAlaAlaLeuValaArgArgPro 389
Db      1315 AGCA-----GCTCGTCTCC 1330

RESULT 7
US-08-331-644-3
; Sequence 3, Application US/08331644
; Patent No. 5976872
; GENERAL INFORMATION:
; APPLICANT: Tao, Wufan
; APPLICANT: Lai, Eseng
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,644
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,292
; FILING DATE: 13-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
```

/	REFERENCE/DOCKET NUMBER:	41472-A-PCt-US
/	TELECOMMUNICATION INFORMATION:	
/	TELEPHONE:	212-278-0400
/	TELEFAX:	212-391-0525
/	INFORMATION FOR SEQ ID NO:	3:
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	1860 base pairs
/	TYPE:	nucleic acid
/	STRANDEDNESS:	single
/	TOPOLOGY:	linear
/	MOLECULE TYPE:	cdna
/	US-08-331-644-3	

Alignment Scores:				
Pred. No.:	2	0.96-1.3	Length:	1860
Score:	404.50		Matches:	133
Percent Similarity:	40.95%		Conservative:	30
Best Local Similarity:	33.42%		Mismatches:	132
Query Match:	19.05%		Indels:	104
DB:	2		Gaps:	13

US-10-087-080-32 (1-402) x US-08-331-644-3 (1-1860)	
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QY	8	ProAgtAlaAhiS-----GjAspLySgInglySerAspLeuIngly	22
Db	245	CCGGCGCTCCGACAGTGTGCGTCTCCGCTCCGGGTCCGCCCTCCGGANTCCGGCTCGGGA	30
QY	23	AlaGlyIserAspAlaProSerProLeuSerAlaAlaGlyAsp-----	37
Db	305	GGCCAGGAGACCGGGAGCCCGGTGCGCTATGTGCGCGCCGACCGCGCCGCCAGC	36
QY	38	---AspSerLeuGlySerAspGlyAspCyS-----	46
Db	365	TATGACCTTGAGAGACGAGATGTCCGATCTCTCCGCTCCGGGAGAGACAGACATCGA	42
QY	47	-----AlaAlaIysProSerAlaGlyIglyIalAarg-AspThrGInglyAspG	63
Db	425	CGTGTGGGGAGGGCGGAGAGACGACGAGAGAGACGATGACGAGAGGGCGCGG	48
QY	63	YGIuGInSerAlaGjYGIglyI-----	70
Db	485	CGGCCCGCGCGCGCGGGGTCCGGTTCGCGAGCTCGGCCAGCGCGGAGCGCTCTTA	54
QY	70	-----	70
Db	545	CGCGGGGAGGTGATCTCGAGAGACTCGAGAGAGAGACAGCATGACTGCTGCTGC	60
QY	71	-----ProGjAlaIaGluGInAlaIleProAlaAlaAlaAlaAlaAlaAlaIaG	88
Db	605	CCCCCGAGCCCGCGCTCCCGCGCCTCCGGGTCTCGCCGCCCGGGGAGCGGGTCT	66
QY	88	uGjAlaIaGInAlaGlyAla-----AlaGjProGjAlaIaGly-----GjAlaIaGlySe	104
Db	665	GGCGGCTGACAGCGCGCGCGAGCGCGCGGAGCGCGCGGAGGTGTACGGGCGCGGCAC	724
QY	104	rgIyGInGjAlaIaIaSerIySProIyTThAArgSPProIySPProIySerIyI	124
Db	725	GGCGCGGGCGCTAAGAAAT-----CGCGTGTG-----AAGCGCGCTTACTGTATCAT	772
QY	124	eAlaIeulIeAlaMeAlaIaIeAArgAspSerAlaGlyIalAargLeuThrIeulAgluI	144
Db	773	CGGCTCATACACATGCGCATCTCGACAGGCCCAAGAGCGCTTACGCTCAGCGAGAT	832
QY	144	eAsnGjUryIleUmeTgLyIySPheProPheArgGlySerIyThrGjYTPArgAS	164
Db	833	CTGCGAGTTCATCAGACAGCCGCTTCTTACTTACCGGAGAAAGTTCCCCGCTTGGCGAA	892
QY	164	nSerValAArgIAsaIeUserIeUasnAspCySPheValIySValIeUArgSPProSe	184
Db	893	CGAGCTCCGTCACAACTGTGTGTCAACGACTGCTTGTCAAGATCCCGCGCAACCGG	952
QY	184	rArgProIrgPglyIySAspAenIyTTrImeIeUasProAsnSerGjUryIyThrIeAl	204

Db 953 CAACCCG---GGCAGAGGCACTACTGAGCGCTCGACCCGCGACTCCGACATATGTTCCA 1009
 QY 204 aaspglyValPheArgArgArgArgArgSerHisArgAlaProValProAlaPr 224
 Db 1010 CAACGGAGAGCTTCTCGGGCGCGCAAGCGCTTCAAG---CGCCAGCGCTACTCGATCC 1066
 QY 224 oglyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProAlaProAla 244
 Db 1067 CGCGCTG----- 1073
 QY 244 aProAlaSerProArgMetArgSerProAlaArgGluGluAlaArgAlaSerProAla 264
 Db 1074 -----GGAGCTCGCACCAAGGAGCAGCGCTGCCAGTGGGA 1111
 QY 264 yLysPheSerSer-SerPheAlaIleAspSerIleLeuArgLysProPheArgSerArg 284
 Db 1112 GAACCTTACTGCTAGGATTT-----CCAAATTGTTAGGACGTCGTAGCGCGGG 1162
 QY 284 rgleuArgAspThrAlaProGlyThrThrLeuGlnTyrGly-----AlaAlaProCysP 302
 Db 1163 AGAGCGAAGTAGAGACTCCGCGCTTCTTCTCCGATGGGGGGGTTGTTTCGTTGCCCC 1222
 QY 302 roProleuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeuPro- 321
 Db 1223 CTCCCGGCTCTCGAGAGACCCCGCGCCC-CGTTTTCGCGCTTCGATTCCTTGACCGAG 1281
 QY 322 -LeuCysAlaTyrGlyAlaGlyLysProAlaArgLeuGlyAlaArg 336
 Db 1282 ACTGTGTGGGCGACAGCTGGGCGCGCGCATTTAGCTCAGAG 1327

RESULT 8

PCT-US93-04102-3

Sequence 3, Application PC/TUS9304102

GENERAL INFORMATION:

APPLICANT: Tao, Mufan

APPLICANT: Lai, Eseng

TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: John P. White

STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/04102

FILING DATE: 19930430

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/862,292

FILING DATE: 13-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41472A-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-977-9550

TELEFAX: 212-664-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1860 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US93-04102-3

Alignment Scores:

Pred. No.: 2,09e-13

Score: 404.50

Percent Similarity: 40.95%

Best Local Similarity: 33.42%

Query Match: 19.05%

DB: 5

Gaps: 13

US-10-087-080-32 (1-402) x PCT-US93-04102-3 (1-1860)

QY 8 ProArgAlaAlaHis-----GlyAspLysGlnLysSerLysLeuGly 22
 Db 245 CGCGGCTGTCACAGATGGCGCTCTCGCTCGGGTCCGCCCTCCGGGATCGCTGGGGA 304
 QY 23 AlaGlyLysSerAspAlaProSerProLeuSerAlaAlaGlyasp----- 37
 Db 305 GGGCAGGAGACCCGAGCCCGGTCCTATGTGCGCGCGCACCGCGCCGCCAGC 364
 QY 38 ---AspSerLeuGlySerAspGlyAspCys----- 46
 Db 365 TATGACCTTAGCAGCAGGAGATGTCGATGCTCCGCGCTCGCGAGAGACAGCATCGA 424
 QY 47 -----AlaAlaLysProSerAlaGlyGlyGlyAlaArg-AspThrGlnGlyaspG 63
 Db 425 CGTGTGGGGAGGGCGAGGACGACGAGGAGGAGAGAGATGACGACGAGGGCGGG 484
 QY 63 yGluGlnSerAlaGlyGlyGly----- 70
 Db 485 CGGCGCGCGCGCGCGCGGTCCTCCGTTCCGAGCTCGGCCAGCGCGAGCGCTCTTA 544
 QY 70 ----- 70
 Db 545 CGCCGCGAGGTGATCTCGAGACTCGAGAGAGAGAGACAGCATGACTGCTGCTGCC 604
 QY 71 -----ProGlyAlaGluGluAlaIleProAlaAlaAlaAlaAlaValValAlaG 88
 Db 605 CCCCCGCGCGCGCGCGTCCCGCGCTCGGGTCCGCGCCCGCGGAGCGGGTGC 664
 QY 88 uGlyAlaGluAlaGlyAla---AlaGlyProGlyAlaGly-----GlyAlaGlySe 104
 Db 665 GGGGCGCTGCGAGCGCGCGCGGAGGCGGCGGAGTGTACGGCGCGGCGAC 724
 QY 104 rGlyGluGlyAlaArgSerLysProTyrThrArgArgProLysProProLysTyr 124
 Db 725 GGGCGGGGCGCTTAGAAT---CCGCTGCTG-----AAGCGGCTTACTGTCAT 772
 QY 124 eAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThrLeuAlaGlu 144
 Db 773 CGCGGTATTCACCAATGGCCATCTGCAGAGGCCCAAGAGGCGCTCAGCGTCAGGAGAT 832
 QY 144 eAsnGlnTyrLeuMetGlyLysPheProPhePheArgGlySerTyrThrGlyTyrArg 164
 Db 833 CTGCGAGTTCATCCAGACCGCGCTTCTTACTTACCGGAGAACTCCCGCTTGCAAGA 892
 QY 164 nSerValArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeuArgAspPro 184
 Db 893 CAGCATCCGTCAACCACTGTGCTCAAGACTGTCTCAAGATCCCGCGGAACCGGG 952
 QY 184 rArgProTyrGlyLysAspAsnTyrTyrMetLeuAsnProLysSerGlyTyrThrPheAl 204
 Db 953 CAACCCG---GGCAGAGGCAACTACTGAGCGCTCGACCCGCGAGTCCGAGATATGTTCCA 1009
 QY 204 aaspglyValPheArgArgArgArgArgSerHisArgAlaProValProAlaPr 224
 Db 1010 CAACGGAGAGCTTCTCGGGCGCGCAAGCGCTTCAAG---CGCCAGCGCTACTCGATCC 1066
 QY 224 oglyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProAlaProAla 244
 Db 1067 CGCGCTG----- 1073
 QY 244 aProAlaSerProArgMetArgSerProAlaArgGluGluAlaArgAlaSerProAla 264


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Db      1074 -----GGGACTCTGACCAAGGACAGCCGCTGTCTCACTGTGGA 1111
Qy      264 YlypPheSerSer-SerPheAlaIleaspSerIleuArgIlyProPheArgSerArg 284
Db      1112 GAACTTACTGCTAGATTT-----CCAAATTGTAGGAAGCTGTTAGCCGCGG 1162
Qy      284 rgluAargAspThrAlaProGlyThrThrIleuGlnTyrGly-----AlaAlaProCysP 302
Db      1163 AGAGCCGAGGTAGGACTCCCGGCTTCTTCTCCGAGTGGGGGGTGTGTTCCGCCCC 1222
Qy      302 rOProIleuProAlaPheProAlaIleuIleuProAlaIleuProCysArgAlaIleuPro- 321
Db      1223 CTCGGGTCCTCGGAGACCCCGCGCCCC-CGGTTTTCGCGCTTGGGATTTCTTGACCAAG 1281
Qy      322 -IleuGlyAlaTyrGlyAlaGlyIleuProAlaIleuArgIleuGlyAlaArg 336
Db      1282 ACTGTGTGGGCGACAGCTGGGGGGCGCGCACTTGTAGCTCAGAGG 1327

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RESULT 9

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US-09-976-594-927
; Sequence 927, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERU Program
; SEQ ID NO 927
; LENGTH: 1309
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6673549 3687719CBI
US-09-976-594-927

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Alignment Scores:

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Pred. No.: 1,63e-13 Length: 1309
Score: 403.50 Matches: 135
Percent Similarity: 44.21% Conservative: 33
Best Local Similarity: 35.53% Mismatches: 136
Query Match: 19.01% Indels: 77
DB: 4 Gaps: 14

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US-10-087-080-32 (1-402) x US-09-976-594-927 (1-1309)

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Qy      75 GtAlaIleProAlaAlaAlaAlaAlaValAlaIleGluGlyAlaGluAlaGlyAl 94
Db      4 GAAAGTGAAGCTGACCCAGCAGAGTCCCAAGACCTGGAGCCCGCAGCATGACGAGC 63
Qy      94 aAlaGly-ProGlyAlaGlyAlaGlySerGlyGluGlyAlaArgSerIlyProIlyT 114
Db      64 AGCCTCTGCGCGGCTGCGCC-----CCACAA 93
Qy      114 hrArgArgProIlyProIlyProIlySerIlyIleAlaIleuIleAlaMetAlaIleArgAsp 134
Db      94 CTGAGCCACCAAGCTCTCTTACAGCTACATCGCCCTTATGTCATGCGCATCCAGACT 153
Qy      134 eAlaGlyIlyArgIleuThrIleuAlaGluIleuGlnIlyIleuMetGlyIlySphProP 154
Db      154 CACGGGGCAGCGGCGCCACCTCAAGTGCATCTTACCGGTATCATGGCGGATTCGGCT 213
Qy      154 hePheArgGlySerIlyThrIlyTyrPArgSerValArgIleAsnIleuSerIleuAsn 174
Db      214 TCTACCGCCACACCGCGCGCTGGCGAGACAGCATCCGCGCACATCTGTCACTCAAGC 273

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Qy      174 spCysPheValIlyValIleuArgAspProSerArgProIlyIlyAspAsnIlyTTrpm 194
Db      274 AGTGTCTTTCATAGTTCGCCCGCATACCGCAAGCA-----GGAAAGGCGAGCTACAGGA 330
Qy      194 etIleuAsnProAsnSerGlyTyrThrPheAlaaspGlyValPheArgArgArgIlysa 214
Db      331 CGCTGACCTGACTGCGACGACATGTTTAGACAGCGCACTTCTTACGCGCGCGGCC 390
Qy      214 rgluSerIly's-ArgAlaProValProAlaProGlyIleuArgProGluGlnAla----- 231
Db      391 GCTTACCCCGGACAGAGTGTAGAGGACCCCGGGCGCCGCCCAAGGACGCGGTGAC 450
Qy      232 ---ProGlyIleuProAla-----AlaProProProAlaProAlaAlaProAla 246
Db      451 CCTCAGGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 510
Qy      247 SerProArgMetArgSerProAlaArgGlnGluIlyArgAla----- 260
Db      511 CATTCCACAG-----AGCTCCAGATCCCAAGGCTTAAGCTTTGGGGGTCTGG 561
Qy      261 ---SerProAlaGlyIlySphSerSerSerPheAlaIleaspSerIleuArgIlyPro 279
Db      562 TGGGGGCGCATGCGACGAGTATGTGCCAGCAACCACTGATGACAGGCTCGGCCACCA 621
Qy      280 PheArgSerArgArgIleuArgAspThrAlaProGlyThrThrIleuGln---TyrGlyAla 298
Db      622 TGGAGGCCAAAGATTT-----CCAGCGCCAGCCTGTGATGCCAGGGAGC 669
Qy      299 AlaProCysProPro---IleuProAlaPheProAlaIleu---IleuProAla----- 313
Db      670 TCCCGTGGCGACCTCATCTTCTCTCA-TGCCAGCGTTTGGCTTCTGCGCGCTTCTCA 728
Qy      314 -----AlaProCysArgAlaIleuIleuProIleuCysAlaTyrGly 326
Db      729 GAGCTGAGATTTAATAAGGCCCTTACGCCGCTGTCTCCCGGAATCAGCATCGGG 788
Qy      327 AlaGlyIleuProAlaArgIleu----- 333
Db      789 AGCAGCTACAGTGTGCGCTGACGACCTGAATTTTGCATGGGGCTGACCCAGGCTT 848
Qy      334 -----GlyAlaArgGluAlaGluValProProThrAlaProProIleu 348
Db      849 GAGCACTTCTGCGCTGACAGACCCCTCCCTGACACACCCACCTCCAGGCTCCTC 908
Qy      349 LeuAlaProIleuProAlaAlaAlaProAlaIlyProIleuArgIlyProAlaIlyGly 368
Db      909 CGGGCCCACTGCGCC-----CTGCCAAGTGCACCAAGAAACCTGGGTTGACAGTGGC 962
Qy      369 AlaHisIleuTyrCysProIleuArgIleuProAlaAlaIleuGlnAlaIleuValArgArg 388
Db      963 TTCCCTGTCCAGGAGGCTCCGGCTTACCATTTGGGGCTGACCCCTGTGCTTATCCGAGC 1022
Qy      389 ProGly-----ProHisIleuSerIlyProValGlu 398
Db      1023 CCAAGAAATGTTCTTCTTGAATAAAGCAGCTCATCCTCGGCGAGCTCCTGTGAG 1076

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RESULT 10

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US-07-882-292-1
; Sequence 1, Application US/07882292
; Patent No. 5324638
; GENERAL INFORMATION:
; APPLICANT: Tao, Wufan
; APPLICANT: Lai, Eseng
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: John P. White
; STREET: c/o Cooper and Dunham, 30 Rockefeller
; CITY: New York
; STATE: New York
; COUNTRY: USA

```


QY	40	LeuGlySeraspGlyaspCySalAlaAlaLysProSerAlaGlyGlyGlyAlaArgAspThr	59
Db	785	CTTGGAGCGCAAAAGCCAG-----CCAGCGCGCGGCGCTGGAGCTGGCGCC	832
QY	60	GlnGlyAspGlyGlnGlnSerAlaGlyGlyGlyProGlyAlaGlnGlnAlaIleProAla	79
Db	833	GTCGGGCGGACGACGAAGGAAGGAGGGCGGGCGCTGGGGGGAGAG-----	880
QY	80	AlaAlaAlaAlaAlaValAlaAlaGlnGlyAlaGlyAlaGlyAlaAlaGlyProGlyAla	99
Db	881	-----AACAAAGGGCGCGGCGCAAGCGCGGCAAG	907
QY	100	GlyGlyAlaGlySerGlyGlnGlyAlaArgSerLysProTyrThrArgArgProLysPro	119
Db	908	GACGGGAGGGGGGCGCAGAGGGC-----GACAAAGAACACGGCAAGTACGAAGAGCCG	961
QY	120	ProTyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyArgLeu	139
Db	962	CGCTTACCTTAACCGCGCTCACTGAAGGGCATCAGACAGTCCGACGAAGCCCTG	102
QY	140	ThrLeuAlaGluIleAsnGlnTyrLeuMetGlyLysPheProPheArgGlySerTyr	159
Db	1022	ACGCTCAACGGCATCTACAGGTTCATCAGAAAGACTTCCCTTACTACCGCGAAGAACAG	108
QY	160	ThrGlyTyrArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLysVal	179
Db	1082	CAGGGGTGGCAAACTTCATCCGCGCAAACTGTCCCTCAACAAGTCTTGAAAGGTA	114
QY	180	LeuArgAspProSerArgProTyrGlyLysAspAsnTyrTrpMetLeuAsnProAsnSer	199
Db	1142	CGGCGCCACTACGACGACCCG---GCAAGGGCAACTCTGATCTGGACCGCTCGAC	119
QY	200	GlnTyrThrPheAlaAspGlyVal-----PheArgArgArgLysArgLeuSer	216
Db	1199	GACGACGTTCATCGGGCGACGACCGGCAAGCTCGGCGCGCTC-CACCACGCTTG	125
QY	217	HisAlaGlnAlaProValProAlaProGlyLeuArgProGlnGlnAlaProGlyLeuProAla	236
Db	1258	GCGCAAGTACCTTTAAGCCCGGGC-----ACG	128
QY	237	AlaProProProAlaProAlaAlaProAlaSerProAlaMetArgSerProAlaArgLys	256
Db	1288	GCTCA-CTTCCA-----CGGCTCACTTCATGACGCGCGCGCT-----	1328
QY	257	GlnGlnArgAlaSerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeu	276
Db	1329	---CCCTCTACTGGCCATGT-----	1346
QY	277	ArgLysProPheAlaArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrp	296
Db	1347	-----CGCCCTTCCTGCTCCCTGCACACACCTCGCGCA	1379
QY	297	GlyAla-----AlaProCysProProLeuProAlaPheProAlaLeuLeu	311
Db	1380	GCAACACTTTCAGTTTACAACGGACACCTTCGCTTACCCACGACACCCCATGC-----	1433
QY	312	ProAlaAlaProCys-----ArgAlaLeuLeuProLeu-----	322
Db	1434	CCTACAGCTCGGTGTGACTCAAAACTCGCGGGGCACAAACCACTCTTCTCCACCGCA	1493
QY	323	-----CysAlaTyrGlyAlaGlyGlnProAlaArgLeuGlyAla	335
Db	1494	ACGGGCTGAGCGTGACCGGCTGTGTCAACGGGGAGATCCCGTACGCCACGACCACTCA	1553
QY	336	ArgGlnAlaGlnValProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAla	355
Db	1554	CGCGCGGTGGCTTCGCGCTCCGTCGCTTCGCGGCTGTGGTGCCTTCGTCGGGACT	1613
QY	356	AlaProAlaLysPro-LeuArgGlyProAlaAlaGlyAlaHisLeuTyrCysProLe	375
Db	1614	ACTCCCTCAACCCCTGCTCGGTCAACTGTTCGCGGGCCAGACCAAGTTACTTTTCCCC	1673

QY 323 -----CysAlaTyrGlyAlaGlyGluProAlaArgLeuGlyAla 335
Db 1494 ACGGGCTGAGGTGAGCGGCTGCTCAACGGGGAGATCCCGTACGCCACGCCACCTCA 1553
QY 336 ArgGluAlaGluValProProThrAlaProProLeuLeuAlaProLeuProAlaAla 355
Db 1554 CGGCGCTGCGCTCGCGCTCGCTCGCGCTCGCGCTCGCGCTCGCGCTCGCGCTCGCGCT 1613
QY 356 AlaProAlaLysProLeuArgGlyProAlaAlaGlyAlaHisLeuTyrCysProLe 375
Db 1614 ACTGCTCAACCCCTGCTCGCTCAACCTGCTCGCGGCGAGACCACTTCTTTTCCCC 1673
QY 375 uArgLeuProAlaAlaLeu-----GlnAlaAlaLeuValArgArgProGlyPr 391
Db 1674 AGCT---CCGCAACCCGCTCAATGATCTTCGACGACGACGACGCTGACGCGCGCG 1730
QY 391 ohisLeuSerTyr 395
Db 1731 CGTCTCTCTCTAC 1743

RESULT 13
US-08-331-644-4
; Sequence 4, Application US/08331644
; Patent No. 5976872
; GENERAL INFORMATION:
; APPLICANT: Tao, Wufan
; APPLICANT: Lai, Bseeng
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,644
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,292
; FILING DATE: 13-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41472-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-331-644-4

Alignment Scores:
Pred. No.: 2.72e-11 Length: 1155
Score: 360.50 Matches: 116
Percent Similarity: 45.27% Conservative: 37
Best Local Similarity: 34.32% Mismatches: 118
Query Match: 16.98% Indels: 67
DB: 2 Gaps: 13

US-10-087-080-32 (1-402) x US-08-331-644-4 (1-1155)
QY 26 SerAspAlaProSerPro---LeuSerAlaAlaGlyAspAspSerLeuGlySerAspGly 44
Db 207 TCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 266
QY 45 AspCysAlaAlaLysProSerAlaGlyGlyAlaArgAspThrGlnGlyAspGlyGlu 64
Db 267 GACCGGCGCTCTGACACAGCATGACAGGCGC-----TTACTCGGTATCGAGCC 317
QY 65 GlnSerAlaGlyGlyGly-ProGlyAlaGluGluAlaIleProAlaAlaAlaAlaAla 84
Db 318 CAACACCTGGAGAGTGTACCTTATGAGTAGAGAAACTACTACCGGCGCGCGGAG 377
QY 84 aValValAlaGluGlyAlaGluAlaGlyAlaAlaGlyProGlyAlaGlyAla----- 102
Db 378 CTAC-----GGCGGATGGCGAGCCCATGCGGCTACTCTCGCGCCACCGAGCA 428
QY 103 ---GlySerGlyGlyAlaAlaArgSerLysProTyrThrArgArgPro----- 117
Db 429 GTACGCGCGCGGATGGCGCGCTCTCTACCGCGCTTACACCATCAGCGCTTTTCTCCAA 488
QY 118 -----LysProProTyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSe 134
Db 489 GGAAGCTGTGAAGCGCGCTTACAGCTATATAGGCTCATACCATGCGCATCGAAGCG 548
QY 134 rAlaGlyAlaGluLeuThrLeuAlaGluIleAsnGlyTyrLeuMetGlyLysFheProPh 154
Db 549 GCGAGAGAAAGATGATCTCTAAGCGCATCTACACGATCATCATGACGTTTCCCTT 608
QY 154 ePheArgGlySerTyrThrGlyTyrPheArgAsnSerValArgHisAsnLeuSerLeuAsn 174
Db 609 CTACCGCGAGAACAGACAGAGCGCTGCGAGAACAGCATCCCGACACTGCTCTCAATGA 668
QY 174 pCysPheValLysValLeuArgAspProSerArgProTyrGlyLysAspAsnTyrTrpMe 194
Db 669 GTGCTTCTGTAAGAGTGGCGCGAGCAAGAAAGCG---GGCAAGGAGAGCTACAGAC 725
QY 194 tLeuAsnProAsnSerGlyTyrThrPheAlaAspGlyValPheArgArgArgLysAr 214
Db 726 GCTCAACCGGAGCTCTCAACATGTTGAGATGAGCACTTCTGCGCGCGCGCGCG 785
QY 214 gLeuSerHisArgAlaProValProAlaProGlyLeuArgProGluGlu-AlaProGlyL 234
Db 786 CTTCAG---AAGAAGATGTGCTCCAGAGAC-----AAGAAGAGCGGCTCAGCT 833
QY 234 euProAlaAlaProProProAlaProAlaAla----- 244
Db 834 CAAGAGCGCGCTCTGACCAAGCGGCGCTCGACAGGAGCCCGGTAGCTGACG 893
QY 245 --ProAlaSerProArgMetArgSerProAlaArgGlnGlu-----A 259
Db 894 GCCAAGAGAGCGCGAAGAAAGTGTGTAAAGCAGAGCGCGCTCCCGCATGCG 953
QY 259 rGAlaSerProAlaGlyLysPheSerSerPheAlaIleAspSerIleLeuArgLysP 279
Db 954 GGTATATCA----- 964
QY 279 ropPheArgSerArgArgLeuArgAspThrAlaProGlyTyrThrLeuGlnTrpGlyAla 299
Db 965 -----AGGTGAGAGCGCTGAGCGCGAGGAGCGCTGACGAGCCAGTCCGG 1010
QY 299 lAProCysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaL 319
Db 1011 CAGGCGATCTTCCAGCGCGCGAGTGTCC-----CAGACGCTGCTGCGCGAGCA 1061
QY 319 euLeuProLeu-----CysAlaTyrGlyAlaGlyGluProAla 331
Db 1062 CCAGCGCGCGCGCTTAAAGCGGCTGCGCGCTTAAAGCGGAGACATCA 1111

RESULT 14
PCT-US93-04102-4
; Sequence 4, Application PC/TUS9304102

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GENERAL INFORMATION:
APPLICANT: Tao, Wufan
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
NUMBER OF INVENTIONS: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: John P. White
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04102
FILING DATE: 19930430
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-04102-4

Alignment Scores:
Pred. No.: 2.72e-11 Length: 1155
Score: 360.50 Matches: 116
Percent Similarity: 45.27% Conservative: 37
Best Local Similarity: 34.32% Mismatches: 118
Query Match: 16.98% Indels: 67
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US-10-087-080-32 (1-402) x PCT-US93-04102-4 (1-1155)
QY 26 SerAspAlaProSerPro--LeuSerAlaAlaGlyAspAspSerLeuGlySerAspGly 44
DB 207 TCCTGCTCTCTGCTCGCGGCTCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 266
QY 45 AspCysAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 64
DB 267 GACCGGCGGCTCTGGGACACAGCATGCGCGCGG-----TTACTCGGTATCGGACCC 317
QY 65 GlnSerAlaGlyGlyGly-ProGlyAlaGluGluAlaLeuProAlaAlaAlaAlaAla 84
DB 318 CAACACCTCTGGAGTGTACCTATTGATGAGCAAAACTACATACCGGCGCGCGCGGAG 377
QY 84 aValValAlaGluGluAlaGluAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 102
DB 378 CTAC-----GGCGGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCA 428
QY 103 ---GlySerGlyGluGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 117
DB 429 GTACGGCGCGCGCGCGCGCGCTCTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 488
QY 118 -----LysProProTyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSe 134

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DB 489 GGACCTGTGTAAGCGCCCTACAGCTATATAGCGCTCATACCAATGCGCATCAGAACCC 548
QY 134 rAlaGlyGlyArgLeuThrLeuAlaGluIleAsnGluTyrLeuMetGlyLysPheProh 154
DB 549 GCCAGAGAAAGATGACTCTTAACGCGCATCTCAACGATTCACGATTCAGACCGTTCCCTT 608
QY 154 ePheArgGlySerTyrThrGlyTyrPArgAsnSerValArgHisAsnLeuSerLeuAsnAs 174
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QY 174 pCysPheValLysValLeuArgAspProSerArgProTyrGlyLysAspAsnTyrTyrPhe 194
DB 669 GTGCTTCGTGAAGATGCGCGCGCGAGCAACAGAACCGG-----GGCAAGGCGAGCTACGAGC 725
QY 194 tLeuAsnProAsnSerGluTyrThrPheAlaAspGlyValPheArgArgArgLysArg 214
DB 726 GCTGACCGCGAGCTCTTAACAATGTTCCAGATGAGACGCTTCGCGCGCGCGCGCGCGG 785
QY 214 gLeuSerHisArgAlaProValProAlaProGlyLeuArgProGlyGlu-AlaProGlyL 234
DB 786 CTTCAG---AAGAAAGATGTGCCAAGAC-----AAGAGAGAGCGGCGCCACT 833
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QY 245 --ProAlaSerProArgMetArgSerProAlaArgGlnGlu-----A 259
DB 894 GCCCAAGAGAGCGCGAAGAAAGTCTGTGTTAAGACGAGCGCGCGCTCCCGCACATGCC 953
QY 259 rGAlaSerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysP 279
DB 954 GTCATCACCA----- 964
QY 279 rObPheArgSerArgGlyLeuArgAspThrAlaProGlyThrThrLeuGlnTyrGlyAla 299
DB 965 -----AGGTGAGAGCGCTGAGCGCGCGAGGAGCGCGCTGAGCGCGCGCGG 1010
QY 299 lArProCysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAla 319
DB 1011 CAGCGCATCTCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1061
QY 319 eLeuProLeu-----CysAlaTyrGlyAlaGlyGluProAla 331
DB 1062 CCAGCGCGCGCGCGCTTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1111

RESULT 15
US-09-976-594-495
Sequence 495, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 495
LENGTH: 5080
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incycle ID No. 6673549 206866.1
NAME/KEY: unsure
LOCATION: 2468
OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-495

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Alignment Scores:

Pred. No.:	1,06e-08	Length:	5080
Score:	324.50	Matches:	106
Percent Similarity:	44.55%	Conservative:	29
Best Local Similarity:	34.98%	Mismatches:	88
Query Match:	15.28%	Indels:	81
DB:	4	Gaps:	11

US-10-087-080-32 (1-402) x US-09-976-594-495 (1-5080)

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QY 129 MetAlaIleArgAspSer-AlaGlyGlyArgLeuThrLeuAlaGluIleAsnGluTyrle 148
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QY 148 uMetGlyLysPheProPhePheArgGlySerTyrThrGlyTyrPArgAsnSerValArgH 168
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QY 168 sAsnLeuSerLeuAsnAspCysPheValIysValLeuArgAspProSerArgProTyrPgl 188
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QY 188 YLysAspAsnTyrTyrMetLeuAsnProAsnSerGluTyrThrPheAlaAspGlyValPh 208
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QY 208 eArgArgArgArgLysArgLysSerHisArgAlaProValProAlaProGlyLeuArgPr 228
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QY 268 rSerPheAlaIleAspSerIleLeuArgLysProPheArgSerArgArgLeuArgAspTh 288
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Db 446 -----CGAGTTGAAGACTCCAGGCTCC 468
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QY 288 r-----AlaProGlyThrThrLeuGlnTyrPglYAlaAlaPro---Cy 301
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Db 469 TCACTGCGCCCCCACTAAAGCTCCGCGCGCG-----GGCGCTGCGCTCTGTG 516
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QY 301 sProProLeu-ProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeuP 321
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Db 517 CCGGCTCTCAACCGCG----- 533
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QY 321 rLeuGlyAlaTyrGlyAlaGlyGluProAlaArgLeuGlyAla---ArgGluAlaGlu 340
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Db 534 -----ACAGGCTTGGCACCCCGACGAGTCCAGCTG 564
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QY 340 aProProThrAlaProProLeuLeuAlaPro----- 351
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Db 565 CACCTGAAGGGGACCCCACTACTCTTCAACCAACCGTTCTCATCAACAACTCATG 624
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QY 352 --LeuProAlaAlaAlaProAlaLysProLeuArgGlyProAlaAlaGlyGlyAlaHisL 371
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QY 391 rHis 392
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Db 739 ACCAC 743

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Job time : 115 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 2, 2004, 16:34:39 ; Search time 598 seconds

(without alignments)
3341.467 Million cell updates/sec

Title: US-10-087-080-32

Perfect score: 2123

Sequence: 1 MKLEVFVPRRAHDKQSGSL.....ALVRRPGPHLSYVETLLA 402

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Searched: 3267054 seqs, 2485319735 residues

Total number of hits satisfying chosen parameters: 6534108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.ccl -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10087080@cgn.1.1.221@runat_27082004.104032.13278
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Database:

Published Applications NA:
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19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match length	DB ID	Description
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1	2123	100.0	1209	13	US-10-229-345-9	Sequence 9, Appl1
2	2123	100.0	1209	16	US-10-274-171-9	Sequence 31, Appl1
3	2123	100.0	1209	16	US-10-087-080-31	Sequence 25, Appl1
4	2123	100.0	1209	17	US-10-650-112-9	Sequence 26, Appl1
5	2081.5	98.0	1212	17	US-10-650-112-25	Sequence 26, Appl1
6	1597	75.2	1203	17	US-10-650-112-26	Sequence 26, Appl1
7	1534	72.3	1203	17	US-10-650-112-27	Sequence 26, Appl1
8	1412.5	66.5	1760	12	US-10-152-319A-1814	Sequence 1814, Ap
9	716	33.7	585	13	US-10-027-633-231353	Sequence 231353,
10	716	33.7	585	16	US-10-027-633-231353	Sequence 231353,
11	488.5	23.0	2487	13	US-10-342-887-1045	Sequence 1045, Ap
12	488.5	23.0	2487	13	US-10-172-118-1045	Sequence 1045, Ap
13	488.5	23.0	2487	13	US-10-205-882-135	Sequence 135, App
14	488.5	23.0	5181	12	US-09-969-007A-802	Sequence 802, App
15	487.5	23.0	2271	15	US-10-101-510-133	Sequence 133, App
16	470	22.1	320	9	US-09-833-881-1266	Sequence 1266, Ap
17	466.5	22.0	2187	10	US-09-960-706-947	Sequence 947, App
18	425	20.0	1662	13	US-10-342-887-611	Sequence 611, App
19	425	20.0	1662	13	US-10-172-118-611	Sequence 611, App
20	423	19.9	1662	10	US-09-292-862-1	Sequence 1, Appl1
21	419.5	19.8	2753	15	US-10-007-280A-115	Sequence 115, App
22	411	19.4	2559	13	US-10-342-887-1132	Sequence 1132, App
23	411	19.4	2559	13	US-10-172-118-1132	Sequence 1132, Ap
24	411	19.4	2559	15	US-10-293-582-24	Sequence 24, Appl1
25	411	19.4	3098	15	US-10-198-846-10858	Sequence 10858, A
26	407.5	19.2	1137	15	US-10-029-386-24788	Sequence 24788, A
27	407	19.2	5001	17	US-10-303-635-18	Sequence 18, Appl1
28	406	19.1	2872	9	US-09-969-708-455	Sequence 455, App
29	406	19.1	2872	13	US-10-342-887-1049	Sequence 1049, Ap
30	406	19.1	2872	13	US-10-172-118-1049	Sequence 1049, Ap
31	406	19.1	2872	13	US-10-388-360-310	Sequence 310, App
32	406	19.1	2872	15	US-10-177-293-211	Sequence 211, App
33	405	19.1	3289	17	US-09-963-285-8	Sequence 8, Appl1
34	405	19.1	3289	17	US-10-806-782-1	Sequence 1, Appl1
35	405	19.1	6458	9	US-09-963-285-6	Sequence 6, Appl1
36	403	19.0	2712	9	US-09-963-285-6	Sequence 94, Appl1
37	403	19.0	2712	17	US-10-303-635-94	Sequence 5, Appl1
38	403	19.0	6021	17	US-09-963-285-5	Sequence 95, Appl1
39	403	19.0	6021	17	US-10-303-635-95	Sequence 9, Appl1
40	391.5	18.4	1506	9	US-09-963-285-9	Sequence 4, Appl1
41	391.5	18.4	1506	17	US-10-303-635-4	Sequence 496, App
42	391	18.4	4454	9	US-09-764-887-496	Sequence 496, App
43	391	18.4	4454	15	US-10-073-961-496	Sequence 497, App
44	387	18.2	4450	9	US-09-764-887-497	Sequence 497, App
45	387	18.2	4450	15	US-10-073-961-497	Sequence 497, App

ALIGNMENTS

RESULT 1
US-10-229-345-9
; Sequence 9, Application US/10229345
; Publication No. US20040038220A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; FILE REFERENCE: CMRU-P01-003
; CURRENT APPLICATION NUMBER: US/10/229, 345
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1161)-(1161)
; OTHER INFORMATION: n=a, c, g, or t
US-10-229-345-9

Alignment Scores:


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QY 101 GYAlAGlySerGlyGluGlyAlaArgSerProThrArgArgProPro 120
Db 301 GGGCGGGGAGCGGCGAGGGGTGACCGACGACCAATATACGGCGCGCCAGACCCCCC 360
QY 121 TySerTyrIleAlaIleuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThr 140
Db 361 TACTGTCATCGCGCTCATCGCAATCGGCAATCGGACCTCGCGGGCGCGGCGCTTGAAG 420
QY 141 LeuAlaGluIleAsnGluTyrLeuMetGlyLysPheProPhePheArgLysSerTyrThr 160
Db 421 CTGGCGGAGATCAACAGATACCTCATGGGCAATTCCTTTTCCGGCGGAGCTACAG 480
QY 161 GlyTPArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeu 180
Db 481 GGCTGGCGCAACTCCGTGGCGCCACAACTTGGCTCAAGACTGCTTCGCAAGGTGCTG 540
QY 181 ArgAspProSerArgProThrProGlyLysAspAsnTyrTyrMetLeuAsnProAsnSerGlu 200
Db 541 CGGACCTCTCGGGCGCTGGGGCAAGCAACTACTGATGCTCAACCCCAACAGCGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgLysArgLeuSerHisArgAlaPro 220
Db 601 TACACCTTGGCGGAGGGGTCTTCCGCGCGCGGAGCGCTCAGCCACCGCGCGCG 660
QY 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGGGGTGGCGCGCGGAGAGGCGCGCGCGCTCCCGCGCGCGCGCG 720
QY 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGluAlaGala 260
Db 721 GGGCGCGCGCGCGCGCTCGCGCGCAAGCGTCCCGCGCGCGCGCGCAAGAGAGCGCGCG 780
QY 261 SerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPhe 280
Db 781 AGCCCGCGGCGCAAGTCTCCAGCTCTCTCGCATGACAGCATCTCTGCGCAAGCCCTTC 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyTyrThrLeuGlnTyrGlyAlaAlaPro 300
Db 841 CCGAGCGCTCGCTCGCGGAGACAGGCGCGCGCGGAGACGACCTTCAGTGGGCGCGCGCG 900
QY 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
Db 901 TCCCGCGCGCTCGCGGTTCCCGCGCTCTCCCGCGCGCGCGCGCGCGCGCGCTGCTG 960
QY 321 ProLeuCysAlaTyrGlyAlaGlyGluProAlaArgLeuGlyAlaArgGlnAlaGluVal 340
Db 961 CCGCTCTGCGGCTACGGCGCGGCGGAGCGCGCGGCTGGCGCGCGGAGCGCGAGGTG 1020
QY 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysPro 360
Db 1021 CCACGCGAGCGCGCGCGCTCTGCTTGCACTCTCCGGCGCGCGCGCGCGCGCAAGCCA 1080
QY 361 LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380
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QY 381 LeuGlnAlaAlaLeuValArgArgProGlyProHisLeuSerTyrProValGlnThrLeu 400
Db 1141 CTGGAGGCGGCTTACTCCGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 1200
QY 401 LeuAla 402
Db 1201 CTAGCT 1206

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RESULT 3

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US-10-087-080-31
; Sequence 31, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.

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; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087, 080
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: winged helix/forhead transcription factor (HNF1)
; NAME/KEY: modified_base
; LOCATION: (1161)
; OTHER INFORMATION: n = g, a, c or t
US-10-087-080-31
Alignment Scores:
Pred. No.: 4,77e-153 Length: 1209
Score: 2123.00 Matches: 402
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
US-10-087-080-32 (1-402) x US-10-087-080-31 (1-1209)
QY 1 MetLysLeuGluValPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20
Db 1 ATGAAGTTGAGGTGTCTCTCTCCCTCGCGCGCGCGCGCGGAGACAGAGGCGGTACTG 60
QY 21 GluGlyAlaGlyGlySerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
Db 61 GAGGCGCGGGCGGCGAGCGAGCGCGCGCTGTCGGCGCGCGGAGACACTCCCTG 120
QY 41 GlySerArgGlyAspCysAlaAlaLysProSerAlaGlyGlyGlyValArgAspThrGln 60
Db 121 GGTCTAGATGGGACTGCGCGCGCAAGCGCTCCGCGCGCGCGCGCGCGCGCGCAAGATTCGAG 180
QY 61 GlyAspGlyGluGlnSerAlaGlyGlyGlyProGlyAlaGluGluAlaIleProAlaAla 80
Db 181 GCGCAGCGCGAACAAGATGCGGAGGCGCGCGCGCGCGCGGAGAGGCGATCCCGCAGCA 240
QY 81 AlaAlaAlaAlaValAlaAlaGluGlyAlaGluAlaGlyAlaAlaGlyProGlyValaGly 100
Db 241 GGTGCTGACAGCGGTGTGGCGGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGG 300
QY 101 GlyAlaGlySerGlyGlyGlyAlaArgSerLysProTyrThrArgArgProLysProPro 120
Db 301 GGGCGGGAGCGGCGGAGGTGACAGCAGCAATATACGGCGCGCGCGCGCGCGCGCGCG 360
QY 121 TySerTyrIleAlaIleuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThr 140
Db 361 TACTGTCATCGCGCTCATCGCAATCGGCAATCGGACCTCGCGGGCGCGGCGCTTGAAG 420
QY 141 LeuAlaGluIleAsnGluTyrLeuMetGlyLysPheProPhePheArgLysSerTyrThr 160
Db 421 CTGGCGGAGATCAACAGATACCTCATGGGCAATTCCTTTTCCGGCGGAGCTACAG 480
QY 161 GlyTPArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeu 180
Db 481 GGCTGGCGCAACTCCGTGGCGCCACAACTTGGCTCAAGACTGCTTCGCAAGGTGCTG 540

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QY 181 ArgAspProSerArgProTpgLyAspAsnTyrThrometLeuAsnProAsnSerGlu 200
Db 541 CGGAGCCCTCGGGCCCTG9G9AAGAGCACTACTGATGCTCAACCCCAAGGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgArgLeuSerHisArgAlaPro 220
Db 601 TACACCTTCGCGAGCGGGGCTTCCTCCGCGCGCGCAAGCGCTCAGACCAACCGGCGCG 660
QY 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGCGCGCGCGCGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 241 AlProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGluArgAla 260
Db 721 GCGCGCGCGCGCGCGCGCGCGCGCGATGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 261 SerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPhe 280
Db 781 AGCCCGCGCGGCAAGTCTCCAGCTCTTCGCAATCGACATCCCTGCGCAAGCCCTTC 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTpgLyAlaAlaPro 300
Db 841 CGAGCGCGTGCCTCAGAGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
Db 901 TGCCCGCGCGTGCCTCCGCGCTCCCGCGCTCTCCCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 321 ProLeuCysAlaTyrGlyAlaGlyGluProAlaArgLeuGlyAlaArgGluAlaGlyVal 340
Db 961 CCGCTGCGCGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysPro 360
Db 1021 CCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
QY 361 LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380
Db 1081 CTCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 381 LeuGlnAlaAlaLeuValArgArgProGlyProHisLeuSerTyrProValGluThrLeu 400
Db 1141 CTGAGAGCGCGCGCTTATGCGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 401 LeuAla 402
Db 1201 CTAGCT 1206

RESULT 4
US-10-650-112-9
; Sequence 9, Application US/10650112
; Publication No. US2004010712A1
; GENERAL INFORMATION:
; APPLICANT: MARROWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CMRU-F01-044
; CURRENT APPLICATION NUMBER: US/10/650, 112
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1161)..(1161)

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; OTHER INFORMATION: n is a,t,g or c
US-10-650-112-9
Alignment Scores:
Pred. No.: 4,77e-153
Score: 2123.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 17 Gaps: 0

US-10-087-080-32 (1-402) x US-10-650-112-9 (1-1209)
QY 1 MetLysLeuGluValPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20
Db 1 ATGAAAGTTGAGAGGTGTTCCTCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
QY 21 GluGlyAlaGlyLysSerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
Db 61 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyAlaArgAspThrGln 60
Db 121 GGCTCAGATGGGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 GlyAspGlyGluGlnSerAlaGlyGlyProGlyAlaGluGluAlaIleProAlaAla 80
Db 181 GCGCAGCGCGCAAGAGTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 AlAlaAlaAlaValAlaAlaGluGlyAlaGluAlaGlyAlaAlaGlyProGlyAlaGly 100
Db 241 GCTGCTGACAGCGGTGTGGGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 101 GlyAlaGlySerGlyGluGlyAlaArgSerLysProTyrThrArgArgProLysProPro 120
Db 301 GCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 121 TyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThr 140
Db 361 TACTCGTACATCCGCGTCACTGCGCATGCGCATCGCGCATCGCGCGCGCGCGCGCGCG 420
QY 141 LeuAlaGluIleAsnGluTyrLeuMetGlyLysPheProPheArgGlySerTyrThr 160
Db 421 CTGGCGGAGATCAACGAGTACTCATGAGGCAAGTCCCTCTTTTCCCGGAGCTTACAG 480
QY 161 GlyTyrArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValValLeu 180
Db 481 GGCTGGCGCAACTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 181 ArgAspProSerArgProTpgLyLysAspAsnTyrThrometLeuAsnProAsnSerGlu 200
Db 541 CGGAGCCCTCGGGCCCTG9G9AAGAGCACTACTGATGCTCAACCCCAAGGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgArgLeuSerHisArgAlaPro 220
Db 601 TACACCTTCGCGAGCGGGGCTTCCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGCGCGCGCGCGCGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 241 AlProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGluArgAla 260
Db 721 GCGCGCGCGCGCGCGCGCGCGCGCGCGATGCGCTCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 261 SerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPhe 280
Db 781 AGCCCGCGCGGCAAGTCTCCAGCTCTTCGCAATCGACATCCCTGCGCAAGCCCTTC 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTpgLyAlaAlaPro 300
Db 841 CGAGCGCGTGCCTCAGAGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900

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QY	301	CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu	320
Db	901	TGCGCGCGCGCTGCCGCTTCCCGGCTCTCCCGCGCGCGCTGCAGAGCGCTGCTG	960
QY	321	ProLeuCysAlaTyrSlValaGlyGluProAlaArgLeuSlValaArgSluAlaGluVal	340
Db	961	CGGCTTGCGCGTACGGCGCGGCGAGGCCGCGCGGCTGGGCGCGCGAGCGCGAGGTG	1020
QY	341	ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaTyrPro	360
Db	1021	CCACGACGCGCGCGCCCTCTCGCTTGACACCTCTCCCGCGCGCGCGCCCGGCAAGCCA	1080
QY	361	LeuAlaGgLYProAlaAlaGlyValaHisLeuTyrCysProLeuAlaGlyLeuProAlaAla	380
Db	1081	CTCCAGAGCGCGCGCGCGCGACCTGTACTGCGCCCTGCGAGCTGCGCGAGCC	1140
QY	381	LeuGlnAlaAlaLeuValaArgArgProGlyProAlaLeuSerTyrProValaGluThrLeu	400
Db	1141	CTGCAGAGCGCGCTTAGTCCGAGGTCTCTGACCGCGACCTTGCTGTAACCGGTGAGAGCGCTC	1200
QY	401	LeuAla 402	
Db	1201	CTAGCT 1206	

RESULT 5

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US-10-650-112-25
; Sequence 25, Application US/10650.112
; Publication No. US20040110712A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CWRU-P01-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: HUMAN FOXQ1
US-10-650-112-25

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Alignment Scores:

Pred. No.:	6.94e-150	Length:	1212
Score:	2081.50	Matches:	396
Percent Similarity:	98.51%	Conservative:	1
Best Local Similarity:	98.26%	Mismatches:	5
Query Match:	98.05%	Indels:	1
DB:	17	Gaps:	1

US-10-087-080-32 (1-402) X US-10-650-112-25 (1-1212)

QY	1	ATGAGTTGAGAGGTGTTGCTCCTCGCGCGCCACGGGAGACACAGGACGATGACCTG	60
QY		MelLysIeuGluValPheValProAlaGlyAlaIleAsnSGlyAspLysGlnGlySerAspIeu	20
Db	21	GlnGlyValAlaGlyLysSerAspAlaProSerProLysSerAlaAlaGlyAspAspSerIeu	40
QY	61	GAGGGCGGGGCGGACGACGCGCGCTCCCGCTGTGGCGGCGGAGACGATCCTTG	120
Db		GlySerAspGlyAspCysAlaAla--LysProSerAlaAlaGlyLysGlyValAlaArgAspThr	59
QY	121	GAGTCAGATGGGACCTCGCGCGCAACACCCGCGCGGCGGCGGCGGCGGACGATCCG	180
Db		GlnGlyAspGlyGlnGlnSerAlaAlaGlyLysGlyProGlnValaGlnGluAlaIleProAla	79
QY	181	CCGGGCGACCGCAACAGAGTGGGAGCGCGGCGGCGGCGGAGAGCGCATCCCGACA	240

OY		80	AlAlaIaaIaaIaaIaaValAlAGlUGlYlaGluIaaGlYlaIaaGlYProdlYla	99
Dd		241	GCAcGTGTGCAGCGGTGTGTGGCCGAAGGCCGGAAGCCGGCGCGCAGAAGCTCG	300
OY		100	GIyGIyAlaGlYSerGIyGIuGIyAlaArgSerLySProYrThrArgArgProLySPro	119
Dd		301	GCGCGCGCGGGAACGGCGAAGGTGCACGCGAGAAAGCATATACGGCGGCCAACGCC	360
OY		120	ProYrSerLyTrIleAlaleuIleAlaMetAlalleaArgabSerAlaGIyGIyArgLeu	139
Dd		361	CCCACTCTGTAACAATCGGCTCATCGCATGSCATCCGCACTCGCGCGGGGGGACTTG	420
OY		140	ThrIleuaIaGluIleasngIutyrLeuMetGIyysPheProPhePheArgGIySerTyrr	159
Dd		421	ACGCTGGCGGAGATCAACAGATTACTCATAGSGCAAGTTCCTTTTCGCGCACGTAC	480
OY		160	ThrglyTrpArgaenSerValArgHisAsnLeuSerLeuaenaaPcySPheVallyVal	179
Dd		481	ACGGGCTGGCCCAACTCCGTGCGCACAACTTTTGCTCAACGACTGCTTGTCNAAGTGT	540
OY		180	LeuaArgaSPProsaerArgProTIrGLyllysaspantyrTPMtleuaSPProsaSer	199
Dd		541	CTGGCGCAACCCTTGCGGCTCTGGGGGAGAGAACATCTGAGTGTCAACCCCAACGCG	600
OY		200	GIuTYrThrPheaIaaSPIyValAPheaArgArgArgLySArGLEuSerHIsArgAla	219
Dd		601	GAGTACAACCTTCGCGCAGGGGGTCTTCCGCCGCGCGCAAGCCCTCAGCACACCGCGCG	660
OY		220	ProValAProAlaPProGIyLEuaRgProGIuGIuAlaPProGIyLeuProAlaAlaPPro	239
Dd		661	CCGGTCCC CGCGCCGGCTGCGCGCCGAGAGAGCCCCGGGCTCTCCCGCGCCCGCGCG	720
OY		240	ProAlaPProAlaAlaPProAlaserProArgMerArgSerProAlaArgGIuGIuArg	259
Dd		721	CCCGCGCCCGCGCCCGCGCTCGCCCCGACATGAGCTCGCCCGCGCAAGAGAGGCG	780
OY		260	AlaserProAlaGIyLysPheSerSerSerPheaIalaSPserIleLeuaArgLySPro	279
Dd		781	GCCAGCCCGCGGSCAAGTCTCCAGCTCCTTGCATCGACATCGACTCTCGCAAGCTC	840
OY		280	PheaRgerArGaIdleuaArgASPThralAProGIyThrThrLeuGIrITPGLyAlaAla	299
Dd		841	TTCGCGACCGCGCCCTCTCAGGAGAACAGGCCCCCGAGAGAGCTTCAGTGGGGCGCGCG	900
OY		300	ProCYSPROProLeuPProAlaPheProAlaleuLeuPProAlaAlaProCYSArGAlaLeu	319
Dd		901	CCCTGCCCGCGCTGCCCGCGCTTCCCGCGCTCTCCCGGGGGGCGCTTGCAGGGCCCTG	960
OY		320	LeuPProLeucySaIaYrGIyAlaGIyGIuPProAlaArgLeuGIyAlaArgGIuAlaGIu	339
Dd		961	CTGCGCGCTCTGCGGTAAGCGCGCGGAGCGCGCGCTGGCGCGCGCGCGGAGGCGAG	1020
OY		340	ValPProProThrhIlaPProPProLeuLeuLeuAlaProLeuPProAlaAlaAlaAlaProAlaLys	359
Dd		1021	GTEGCACCGAACCGGGCGCCCTCTGCTTGCACCTTCCCGGGGGGGCCCCCGCAAG	1080
OY		360	ProLeuaRglYPProAlaAlaGIyGIyAlaHiSIeuTYrCySPProLeuaArgLeuProAla	379
Dd		1081	CCAATCCGAAGCCCCGGCGCGCGGGCGCACCTGTACTGCCCTTGGCGGCTGCCGCCA	1140
OY		380	AlAleuGIuAlaAlaLeuValArgArgProGIyProHISLeuSerTyrrProValGIuThr	399
Dd		1141	GCCTCTGACGGCGGCTCATGTCGCCGCCCTTGGCCCGCACCTCGCGTACC GG TGGAGACG	1200
OY		400	LeuLeuAla 402	
Dd		1201	CTCCTTAGCC 1209	

RESULT 6

US-10-650-112-26
; Sequence 26, Application US/10650112
; Publication No. US20040110712A1

```

GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CMRU-P01-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 26
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: MOUSE FOXQ1
; US-10-650-112-26

Alignment Scores:
Pred. No.: 5.63e-113 Length: 1203
Score: 1597.00 Matches: 320
Percent Similarity: 82.27% Conservative: 14
Best Local Similarity: 78.82% Mismatches: 62
Query Match: 17 Indels: 10
DB: Gaps: 6

US-10-087-080-32 (1-402) x US-10-650-112-26 (1-1203)
QY 1 MetLysLeuGluValPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20
DB 1 ATGAAATGGAGGTGTTCTGCCACGGGACCCCGAGCAAAATGGCGACGATCTG 60
QY 21 GlnGlyAlaGlySerAspAlaProSerProLeuSerAlaAlaGlyAspSerLeu 40
DB 61 GAGGGGGCGCGGACGAGCGAGCTGCCATCTCCACTGTCGGCTGGTGCAGCTCTTA 120
QY 41 GlySerAspGlyAspCysAlaAla--LysProSerAlaGlyGlyAlaArgAspThr 59
DB 121 GGCTCAGACGGGACTGTGACGCAACAGCCCGGGCGGCGGCGGCGGATCTG 180
QY 60 Gln---GlyAspGlyGlnSerAlaGlyGlyProGlyAlaGlnAlaAlaPro 78
DB 181 GAAAGTGGCGCGCGGAGGAAATCGAGTGGCGGCGGCGGCGGCGGCGGAG 240
QY 79 AlaAlaAlaAlaAlaAlaValAlaGlnGlyAlaGlnAlaAlaGlyProGly 98
DB 241 GCAACTGATGACAGACA-----ACGCAAGCTCTCCGGCGAGGCGCTGC 285
QY 99 AlaGlyGlyAlaGlySerGlyGlnGlyAlaArgSerProThrArgAspProLys 118
DB 286 GCGGGCGCGGTGGCGGCGGAGGGGCGGCGAGCGGCAACGCGGCGGCGCAAG 345
QY 119 ProProTyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyArg 138
DB 346 CCCCACACTCTCAATCGCTCTCATGGCCATCCGCACTCCGGGGGAGAGCG 405
QY 139 LeuThrIleAlaGlnIleAsnGluTyrLeuMetGlyLysPheProPheArgGlySer 158
DB 406 CTGACACTGGCCGAGATCAAGATCACTCATGGGCAAGTTCCCTTTTCCGGGCGAGC 465
QY 159 TyrThrGlyTrpArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLys 178
DB 466 TACACGGGCTGGGCAACTCCGTGGCCACAACTCTCGCTCAACGACTGTTTCGTAAG 525
QY 179 ValLeuArgAspProSerArgProTyrGlyLysAspAsnTyrTrpMetLeuAsnProAsn 198
DB 526 GTGCTGGCAACCCCTCGGGCGCTGGGGGCAAGACAACACTGAGATGCTCAACCCCAAC 565
QY 199 SerGlnTyrThrPheAlaAspGlyValPheArgTrpArgTrpArgLysLeuSerHisArg 218
DB 586 AGCGAATACACCTTCGCGCAAGGGGTCTTCGCGCGCGGCGCAAGCGCTCAACGACCGG 645

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QY 219 AlaProValProAlaProGlyLeuAsnProGlnGlnAlaProGlyLeuProAla---Ala 237
DB 646 ACCACAGTCTCCGGCGCGGGCTGGCGGAGGAAAGCCCAACCGGACTCTCCGGGAGC 705
QY 238 ProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGlu 257
DB 706 CCGAGACCGCGCGCGCGCGCGCTCCCGGATCGCGCGCTCGCGCGGCTCGCCAGAG 765
QY 258 GlnArgAlaSerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuArg 277
DB 766 GAGCGCTCCAGCGCTCGGAGCAAGTCTCACTCTTCGATGACAGCAATTCACAGC 825
QY 278 LysProPheArgSerArgTrpArgAspThrAlaProGlyThrThrLeuGlnTrpGly 297
DB 826 AAGCTTTTCGACAGCGCGCGGACCGGCGGACTGCTGCGCGCTGAGCTACCCCTGGGG 885
QY 298 AlaAlaProCysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArg 317
DB 886 GCGGCTCCCTGCGCGCGCTGGCGGCTATCCCGGCTCTTCCGCGCGCGCGGTGGC 945
QY 318 AlaLeuLeuProLeuCysAlaTrpGlyAlaGlyGlnProAlaArgLeuGlyAlaArgGln 337
DB 946 GCTCTGCTACCGCTCTGTCTTACGCGGCAACGAGCTTACCTGCTGCGCGTGGCGG 1005
QY 338 AlaGluValProProThrAlaProProLeuLeuAlaProLeuProAlaAlaAlaPro 357
DB 1006 ACCGAGGTGACGCGCGGCGG---CCCTCTGCTGGCGCCCTCTCCACCGGCGCTCCA 1062
QY 358 AlaLysProLeuAlaArgLysPro--AlaAlaGlyAlaHisIleuTyrCysProLeuArg 376
DB 1063 GCCAAGCCATTCGAGAGTCCGAGACCGCGGCGGCGGCGCACTGATGACCCCTTACCG 1122
QY 377 LeuProAlaAlaLeuGlnAlaAlaLeuValArgArgProGlyProHisIleuSerTyrPro 396
DB 1123 CTGCCACGCGCGCTGCGAGCGGCGAGCGGCTGGTCCGATCGGACCTGTCATCCCG 1182
QY 397 ValGlnThrLeuLeuAla 402
DB 1183 GTGGAGACTCTGCTAGCT 1200

RESULT 7
US-10-650-112-27
; Sequence 27, Application US/10650112
; Publication No. US20040110712A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CMRU-P01-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 27
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: RAT FOXQ1
; US-10-650-112-27

Alignment Scores:
Pred. No.: 3.55e-108 Length: 1203
Score: 1534.00 Matches: 311
Percent Similarity: 79.90% Conservative: 15
Best Local Similarity: 72.23% Mismatches: 68
Query Match: 17 Indels: 14
DB: Gaps: 7

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US-10-087-080-32 (1-402) x US-10-650-112-27 (1-1203)

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QY      1 MetLysLeuGluValPheValProAlaGAlaAHISGLYAspLysGlnGlySerAspLeu 20
Db      1 ATGAATAATTGAGGTATTGCCCCACGCGACGCCAAGGGGACAAAGTGGGCACTGACCTG 60
QY      21 GluGluValAGlySerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
Db      61 GAGGGGGCCGCGACGCGACGCGCATCTCCGCTGTCGCGGCTGGCGACGACCTCTTA 120
QY      41 GlySerAspGlyAspCysAlaAla---LysProSerAlaGlyGlyValAlaArgSpThr 59
Db      121 GGCTCTGACGGGAGCTGTGTACGCCAACGCCCGCGCGGCGAGAGGCCCTGTGATCTG 180
QY      60 Gln---GlyAspGlyGluGlnSerAlaGlyGlyGlyProGlyValaGluAlaAlaIlePro 78
Db      181 GAAAGGGGGGGGCGGAGAGGAATTGAGTGGCGGGGCGAGACGCCAAC----- 231
QY      79 AlaAlaAlaAlaAlaValAlaAlaGluGlyAla-----GluAlaGlyAlaAlaGly 96
Db      232 -----GATCCCGAGGTGACCCGATGCGACAGAACGACGCTCCCGGTGGGG 279
QY      97 ProGlyAlaGlyGlyAlaGlySerGlyGlyGlyAlaArgSerLysProThrArgArg 116
Db      280 CGTGGCGGGGCGAGCGTGGCGCGGTGAGGGCGGCGGAGAGCGCTGACAGCGGCGG 339
QY      117 ProLysProProTySerTyIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGly 136
Db      340 CCCAAGCCCCCTACTCTCATCTGACATCGCATCGCATCGCATCGGACCTCCGCGGCG 399
QY      137 GlyAlaGluThrLeuAlaGluIleAsnGlyLysMetGlyLysPheProPheArg 156
Db      400 GGAGCGCTGACCGCTGGCGCGAGATCAACGAGTACCTATGGGCAAGTCCCTTTTCCGG 459
QY      157 GlySerTyThrGlyThrArgAsnSerValArgHISAsnLeuSerLeuAsnAspSerPhe 176
Db      460 GSGAGCTACAGGGGCTGGCGCACTCCGCGCGCAACACTCTCGCTCAACACAGTGTTC 519
QY      177 ValLysValLeuArgAspProSerArgProTProGlyLysAspAsnTyThrMetLeuAsn 196
Db      520 GTCAAGTCTCTCGGACCCCTCGCGGCTCGGGCGAGAGAAATTACTGAGTCTCANC 579
QY      197 ProAsnSerGlyTyThrPheAlaAspGlyValPheArgArgArgArgLysArgLeuSer 216
Db      580 CCCAACAGGGAATPACCTCTCGCGACGGGGGCTTCCGCGCGCGGCGAAGCGCTCAGC 639
QY      217 HisArgAlaProValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAla 236
Db      640 CACCGGACCAAGTCTCGCATCGGGGCTACGCGCGAGAGAGCCCAACCCCGACCTGGG 699
QY      237 ---AlaProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArg 255
Db      700 GGGACCCCGGACCCCGCGCCACCGCGGCTCTCCCAATGCGCGGCTCGCGCTCGC 759
QY      256 GlnGluGluValArgAlaSerProAlaGlyLysPheSerSerPheAlaIleAspSerIle 275
Db      760 CAGGAGGAGGCGCTCCAGCGCGCGAGCAAGTCTCAGGCTCTTCCGCAATCGACGATC 819
QY      276 LeuArgLysProPheArgSerArgArgLeuArgArgPThrAlaProGlyThrThrLeuGln 295
Db      820 CTCAGCAAGCGCTTTCGACGCGCGCGAGCGGCGACCGGCTCTGGGGGTGACGCTACCC 879
QY      296 TrpGlyAlaAlaProCysProProLeuProAlaPheProAlaLeuLeuProAlaAlaPro 315
Db      880 TGGAGCGCTGCTCTCTGCGCGCGCGCTGATCCGCGCTCTTCCCGCGTGTGCC 939
QY      316 CysArgAlaLeuLeuProLeuCysAlaArgGlyAlaGlyLysProAlaArgGluGlyAla 335
Db      940 GCGGGTGCCCTGCTCCGCTGTGTCTTACGCGCGGCGAGACCCACGCTGTGCGCTGC 999
QY      336 ArgGlyAlaGluValProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAla 355
Db      1000 GCGGGGGCGAGGTGAGCCCGCGGCG---CCCTGTGTCTGGCGCCCTCTTCCACCGCG 1056

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QY      356 AlaProAlaLysProLeuArgGlyPro---AlaAlaGlyGlyAlaHisLeuTyrcysPro 374
Db      1057 GCCCGAGCGCAAGCATTTTCGAGGTCCGAGAGACCGCGCGCGGCGACCTGTACTGCCCC 1116
QY      375 LeuArgLeuProAlaAlaLeuGlnAlaAlaLeuValArgArgProGlyProHisLeuSer 394
Db      1117 CTACCGCTGCCACCGCCCTTCGAGGCGGCGCGCTGGCGGTCCGAGTCCGACCTGTCC 1176
QY      395 TyrProValGluThrLeuLeuAla 402
Db      1177 TACCGGTGGAGACGCTGCTAGCT 1200

RESULT 8
US-10-152-319A-1814
/ Sequence 1814, Application US/10152319A
/ Publication No. US20040072160A1
/ GENERAL INFORMATION:
/ APPLICANT: Mendrick, Donna
/ APPLICANT: Porter, Mark
/ APPLICANT: Johnson, Kory
/ APPLICANT: Higgs, Brandon
/ APPLICANT: Castle, Arthur
/ APPLICANT: Elashoff, Michael
/ TITLE OF INVENTION: Molecular Toxicology Modeling
/ FILE REFERENCE: 44921-5089-US
/ CURRENT APPLICATION NUMBER: US/10/152,319A
/ CURRENT FILING DATE: 2002-05-22
/ PRIOR APPLICATION NUMBER: US 60/292,335
/ PRIOR FILING DATE: 2001-05-22
/ PRIOR APPLICATION NUMBER: US 60/297,523
/ PRIOR FILING DATE: 2001-06-13
/ PRIOR APPLICATION NUMBER: US 60/298,925
/ PRIOR FILING DATE: 2001-06-19
/ PRIOR APPLICATION NUMBER: US 60/303,810
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 60/303,807
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 60/303,808
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 60/315,047
/ PRIOR FILING DATE: 2001-08-28
/ PRIOR APPLICATION NUMBER: US 60/324,928
/ PRIOR FILING DATE: 2001-09-27
/ PRIOR APPLICATION NUMBER: US 60/330,867
/ PRIOR FILING DATE: 2001-11-01
/ PRIOR APPLICATION NUMBER: US 60/330,462
/ PRIOR FILING DATE: 2001-10-22
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2221
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1814
/ LENGTH: 1760
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. NM_022858
US-10-152-319A-1814

Alignment Scores:
Pred. No.: 9,12e-99 Length: 1760
Score: 1412.50 Matches: 300
Percent Similarity: 77.64% Conservative: 16
Best Local Similarity: 73.71% Mismatches: 78
Query Match: 66.53% Indels: 17
DB: 12 Gaps: 6

US-10-087-080-32 (1-402) x US-10-152-319A-1814 (1-1760)
QY      1 MetLysLeuGluValPheValProAlaGAlaAHISGLYAspLysGlnGlySerAspLeu 20
Db      207 ATGAATAATTGAGGTG-TTGTCTCCACGCGCGACG-CACGGGGAACAAATGGGACGCACTCG 264

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QY	21	GlulGlyAlaGlyGlySerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu	40
Db	265	GAGGGGGCGGCGACGACGACGAGCTGCCATCTCCATCTCCGGCGCTGGTGAACATCTCTTA	324
QY	41	GlySerAspGlyAspCysAlaAla---LysProSerAlaGlyGlyAlaArgAspThr	59
Db	325	GGCTCAGACGGGGACTGTGTGACGCCAACAGCCCGGGGGCGGCGAGGGCGCGGGGATCTG	384
QY	60	Gln---GlyAspGlyGluGlnSerAlaGlyGlyGlyProGlyAlaGluGlnAlaLeuPro	78
Db	385	GAAAGTGGCGGGCGAGAGGAATTCAGTGGCGGGCGGAGACCCCAAGAC-----	435
QY	79	AlaAlaAlaAlaAlaAlaValAlaGluGlyAla-----GluAlaGlyAlaAlaGly	96
Db	436	-----GATCCGAGGTGACCGATGGACAGACAGACAGCGCTCCCCGGTGGG	483
QY	97	ProGlyAlaGlyGlyAlaGlySerGlyGluGlyAlaArgSerLysProTyrThrArgArg	116
Db	484	CCGTGGCGGGCGAGGTGGGGCGGGGTGAGGGCGGGCGACAGACCGTCAACGGCGGG	543
QY	117	ProLysProProTyrSerTyrTlleAlaLeuIleAlaMetAlaIleArgAspSerAlaGly	136
Db	544	CCCAAGCCCCCTCTCTCTACATGCACTATCGCAATGGCATTCGGCATTCGGCGGGAC	603
QY	137	GlyArgLeuThrLeuAlaGluIleAsnGluTyrLeuMetGlyLysPheProPheArg	156
Db	604	GAGCGCTGAGCGCTGGCGGCAATCAACAGTACTCATGGGCAAGTTCCCTCTTTCCGG	663
QY	157	GlySerTyrThrGlyTyrPArgAsnSerValaArgHisAsnLeuSerLeuAsnAspCysPhe	176
Db	664	GGCAGCTACACGGGGCTGGCGCACTCCGTGGGCCCAACACTCTGCTCAACGACTGTTTC	723
QY	177	ValLysValLeuArgAspProSerArgProTirpGlyLysAspAspTyrTyrMetLeuAsn	196
Db	724	GTCAAGGTGCTGGCGGACCTCTCGGGCGCTGGGGCAAGCAATTCGATGCTCTCAAC	783
QY	197	ProAsnSerGlyTyrThrPheAlaAspGlyValPheArgArgArgTyrArgLeuSer	216
Db	784	CCCAACACCGAATACACTTGGCGGAGGGGTCTTCCGCGCGCGCGCAAGGCTCTCAAC	843
QY	217	HisArgAlaProValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAla	236
Db	844	CACCGGACACAGTCTCCGCATCGGGCTACGGCGGAGGAGAAGCCACCCGGACCTGGGGG	903
QY	237	AlaProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGln	256
Db	904	ACCCTGGACGCGCGCCACCGCGCGGTCTTCCCAATCGCGCGCTCCGCTCGCTCGCAG	963
QY	257	GluGluAlaGlyAlaSerProAlaGlyLysPheSerSerPheAlaIleAspSerTlleu	276
Db	964	GAGGAGGGCTCCACGGCGGCGGACGACGAAGTCTCCACTCTTCCCATGACGACATCTTC	1022
QY	277	ArgLysProPheArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTyr	296
Db	1024	AGCAAGCCGTTTCGAGCGCGCGGCA---CGGCAACCCGGCTCTGGGGTGGAGTACCTGG	1082
QY	297	GlyAlaAlaProCysProProLeuProAlaPheProAlaLeuProAlaAlaProCys	316
Db	1083	AGCGTGTCTCTGGCGCGCGGTGGGCGCTATCCCGGCGTCTTCCGCGTGTCCGAG	1144
QY	317	ArgAlaLeuLeuProLeuCysAlaArgTyrAlaGlyGluProAlaArgLeuAlaArg	336
Db	1143	GGTGGCCGTGCTCCGCTGTGTCTTACGGCG---GGCGAAGCCACGCTGTGGTGGCGC	1201
QY	337	GluAlaGlyValAlaProThrAlaProProLeuLeuAlaProLeuProAlaAlaAla	356
Db	1202	GGGGCCGAGGTGCAGCCCGCGGCG---CCCTGTTCTGTGGGCCCTCTCCACCGCGGCT	1255
QY	357	ProAlaLysProLeuArgGlyPro---AlaAlaGlyAlaValaAlaLeuTyrCysProLeu	375
Db	1259	CCAGCGAAGCATTTTGAAGTCCGGAGAACCAGCGCGGCGGCGACACTGACTGACCCCTGA	1311
QY	376	ArgLeuProAlaAlaLeuGlnAlaAlaLeuValaArgArgProGlyProHisLeuSerTyr	395

Accession	Gene	Protein	Length	Score	Percent Similarity	Best Local Similarity	Query Match	DB
Db	1319	CGGCTGCCCAAGGCGCTTGCAGAGCGCGCGCTGCGGTCGAGGTCGCACTGTGCTAC	137					
QY	396	ProVal1GluThrLeuAla	402					
Db	1379	CGGGTGAGAGCGCTGCTAGCT	1399					
RESULT 9								
US-10-027-632-231353/c								
; Sequence 231353, Application US/10027632								
; Publication No. US20020198371A1								
; GENERAL INFORMATION:								
; APPLICANT: Wang, David G.								
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide								
; TITLE OF INVENTION: Polymorphisms in the Human Genome								
; FILE REFERENCE: 108827.129								
; CURRENT APPLICATION NUMBER: US/10/027.632								
; CURRENT FILING DATE: 2002-04-30								
; PRIOR APPLICATION NUMBER: US 60/218,006								
; PRIOR FILING DATE: 2000-07-12								
; PRIOR APPLICATION NUMBER: US 60/198,676								
; PRIOR FILING DATE: 2000-04-20								
; PRIOR APPLICATION NUMBER: US 60/193,483								
; PRIOR FILING DATE: 2000-03-29								
; PRIOR APPLICATION NUMBER: US 60/185,218								
; PRIOR FILING DATE: 2000-02-24								
; PRIOR APPLICATION NUMBER: US 60/167,363								
; PRIOR FILING DATE: 1999-11-23								
; PRIOR APPLICATION NUMBER: US 60/156,358								
; PRIOR FILING DATE: 1999-09-28								
; PRIOR APPLICATION NUMBER: US 60/146,002								
; PRIOR FILING DATE: 1999-08-09								
; NUMBER OF SEQ ID NOS: 325720								
; SOFTWARE: FastSeq For Windows Version 4.0								
; SEQ ID NO 231353								
; LENGTH: 585								
; TYPE: DNA								
; ORGANISM: Human								
US-10-027-632-231353								
Alignment Scores:								
Pred. No.: 3,81e-46 Length: 585								
Score: 716.00 Matches: 136								
Percent Similarity: 97.84% Conservative: 0								
Best Local Similarity: 97.84% Mismatches: 3								
Query Match: 33.73% Indels: 0								
DB: 13 Gaps: 0								
US-10-087-080-32 (1-402) x US-10-027-632-231353 (1-585)								
QY	264	GlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPheArgSerArg	283					
Db	583	GGCAGGTTCTCCAGCTCTCTCCGCAATCAGACGACCTTCGGAGACCCCTTCGCGAGCCGC	524					
QY	284	ArgLeuArgAspThrAlaProGlyThrThrLeuGlnTTPGlyAlaAlaProCysPropo	303					
Db	523	CGCCTCAAGGACACGCGCCCGGAGCAGCTTCAGTGGGCGCGCGCCTGCGCGCG	464					
QY	304	LeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeuProLeuCys	323					
Db	463	CTGCCCGCGGTTCCCGCGGCTCTCCCGCGGCGCCTCGAGGGCCTGTGCGCTCTGC	404					
QY	324	AlaTyrGlyAlaGlyGluProAlaArgLeuGlyAlaArgGluAlaGlyAlaProProThr	343					
Db	403	GGGTACGCGCGGCGAGCGCGCGCGCTGGCGCGCGCGAGGTCGACCGAGCC	344					
QY	344	AlaProProLeuLeuLeuAlaProLeuProAlaAlaProAlaLysProLeuArgGly	363					
Db	343	GGCGCGCCCTCTCTCTGCACTCTCCCGGCGGCGCGCCCGCAAGCACTCGAGGC	284					
QY	364	ProAlaAlaGlyAlaAlaHisLeuTyrCysProLeuArgLeuProAlaAlaLeuGlnAla	383					
Db	283	CGGCGCGCGCGCGCGCGCACTGTACTGCCCTCTCGGCTGCCGCAAGCCTCGAGGG	224					

QY	384	AlaLeuValArgArgProGlyProHisLeuSerTyrProValGluThrLeuLeuAla	402
Db	223	GCTCAGTCCGCGCCCTGCGCCGACCTGCGGTACCGGTGGAGAGCGCTCTAGCC	167
RESULT 10			
	US-10-027-632-231353/c		
	Sequence 231353, Application US/10027632		
	Publication No. US20030204075A9		
	GENERAL INFORMATION:		
	APPLICANT: Wang, David G.		
	TITLE OF INVENTION: Identification and Mapping of Single Nucleotide		
	TITLE OF INVENTION: Polymorphisms in the Human Genome		
	FILE REFERENCE: 108827.129		
	CURRENT APPLICATION NUMBER: US/10/027,632		
	CURRENT FILING DATE: 2002-04-30		
	PRIOR APPLICATION NUMBER: US 60/218,006		
	PRIOR FILING DATE: 2000-07-12		
	PRIOR APPLICATION NUMBER: US 60/198,676		
	PRIOR FILING DATE: 2000-04-20		
	PRIOR APPLICATION NUMBER: US 60/193,483		
	PRIOR FILING DATE: 2000-03-29		
	PRIOR APPLICATION NUMBER: US 60/185,218		
	PRIOR FILING DATE: 2000-02-24		
	PRIOR APPLICATION NUMBER: US 60/167,363		
	PRIOR FILING DATE: 1999-11-23		
	PRIOR APPLICATION NUMBER: US 60/156,358		
	PRIOR FILING DATE: 1999-09-28		
	PRIOR APPLICATION NUMBER: US 60/146,002		
	PRIOR FILING DATE: 1999-08-09		
	NUMBER OF SEQ ID NOS: 325720		
	SOFTWARE: FastSeq for Windows Version 4.0		
	SEQ ID NO: 231353		
	LENGTH: 585		
	TYPE: DNA		
	ORGANISM: Human		
	US-10-027-632-231353		
Alignment Scores:			
	Pred. No.:	3,81e-46	Length: 585
	Score:	716.00	Matches: 136
	Percent Similarity:	97.84%	Conservative: 0
	Best Local Similarity:	97.84%	Mismatches: 3
	Query Match:	33.73%	Indels: 0
	DB:	16	Gaps: 0
	US-10-087-080-32 (1-402) x US-10-027-632-231353 (1-585)		
QY	264	GlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPheArgSerArg	283
Db	583	GGCAAGTTCTCCAGCTCTCTCGCATCGACAGCATCTGGCAAGCCCTTCCGACAGCGC	524
QY	284	ArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrpGlyAlaAlaProCysProPro	303
Db	523	CGCCCTCAGGAGAACCGGCCCGCGGAGAGAGCGTTCACTGGGGCGCCGCGCTGCGCGC	464
QY	304	IeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeuProLeuCys	323
Db	463	CTGCCCGCGTTTCCCGCGCTCTCTCCCGCGCGCCCTCTGACAGGGCCCTGCTGCGCTGC	400
QY	324	AlaTyrGlyAlaGlyGluProAlaArgLeuGlyAlaArgGluAlaGluValProProThr	343
Db	403	GGCTACGGCGGGCGAGCGCGCGGCTGGCGCGCGCGRGGCCGAGGTGCACCGACC	344
QY	344	AlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysProLeuArgGly	363
Db	343	GGCGCGCCCTCTGCTGTAACCTCTCCCGCGCGCGCCCGCAAGCACTCCGAGGC	284
QY	364	ProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAlaLeuGlnAla	383
Db	283	CCGGCGCGCGCGCGCGGACGACCTGACTGCCCCCTGGCGGTGCCCGCAGCCCTGACAGCG	224
QY	384	AlaLeuValArgArgProGlyProHisLeuSerTyrProValGluThrLeuLeuAla	402

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Db      223 GCTTCAGTCCGCGCCTTGCGGCCGCACACTGGCGTAACC GGATGAACA CGCTCCTA CCG   167

RESULT 11
US-10-342-887-1045
; Sequence 1045, Application US/10342887
; Publication No. US20040058340x1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPlicant: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188--999
CURRENT APPLICATION NUMBER: US/10/342,887
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1045
LENGTH: 2487
TYPE: DNA
ORGANISM: Homo sapiens
US-10-342-887-1045

Alignment Scores:
Pred. No.:          3,12e+28           Length:         2487
Score:              488.50             Matches:        170
Percent Similarity: 47.56%            Conservative:    35
Best Local Similarity: 39.44%          Mismatches:     147
Query Match:       23.01%               Indels:         83
DB:                13                   Gaps:          20

US-10-087-0880-32 (1-402) x US-10-342-887-1045 (1-2487)

QY      14 AspylsglnglyserAsplrengluaglglgylgySerAspAlaProsePrroIeuSer 33
Dp      : :::::                               |
Sb      506 GAAGAAGAGAGCAAGAACAGAGGCGCGGTGGCGGGCCC-CGGCTGGCTGCCCCCGCGCA 564
QY      34 AlaialagLyaspasPserleuglyserAspglyaSpCyalaAlalysProseralagly 53
Dp      565 GGGGGGCGGGCGCGCGCTCTGTAAGCCGGGAGAGCACGACTGGAGATCTGTAGAGAGGA 624
QY      54 Glylglylaary-AsprThrglnglyAspelyghlugInserlalaglyglyYPproglyal 73
Dp      625 GGAGAGACACGATGACATCTG-----CTGGCCCCGCTGCTGGGGGCTCCCGCGCGCC 678
QY      73 agluGlualalleProAlaalAlaalAlaalavalAlaalagiuglyALagluaLag 93
Dp      679 CCCGGGCCCCGGCCCCGGCGCGGGGCA-----GGAGCCGGTGGGG 720
QY      93 yALAhaLaGIyPROGLyaLAgiLYaLAGlySeR---GYgluGuLYAlarGSerySPr 112
Dp      721 CGGGCGGGCGGGCGGGCGGGCGGGCGGGAGCCGGGTAGCGCGCCAAGAAC--CC 777
QY      112 cTyrrThrArGaRProlYSPrOPrOtyrsertyrlleaLealeuleiaLameaLalleAr 132
Dp      778 GCTGGTG-----AAcCcCCcCTtAcTGMAtatCGcgctacATCATATggCaTTcc 828
QY      132 gAspserralAglyglYargLeuthrleuaLagluileangluTYrleumetclYysph 152
Dp      829 GCAGAGCCCCAAGAACGGCGCTACCGTAGCAAGATTGTGATTATCATCGCGCGCTT 888
QY      152 ePhrophepeARvgLIyseTyrrThrclyYrpARGenSenValArgHIsasnIeusertle 172z
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Db      889 CCCCCTACTACGGGAGAGATTCCCGGCTGAGAGACATCCGCCAACACTCTCGCT 948
Qy      172 uasaspCysPheValIysValLeuArgAspProSerArgProIrrpGlyysAspArg 192
Db      949 CAAAGCTGCTTCTCAAGATCCCCCGAGACCCGGCAACCGG--GGCAAGGGCAACTA 1005
Qy      192 rTTPMeLeuAsnProAsnSerGlyThrPheAlaAspGlyValPheArgArgArg 212
Db      1006 CTGGACCTGGACCCGGAGTCCGCCGACATGTTGACACAGCGAGCTTCTCGGCCGGAG 1065
Qy      212 glyArgLeuSerHisArgAlaProValProAlaProGlyLeuArgProGluAla-- 231
Db      1066 GAAGCGCTTCAAG--CGGACGCGCTGCTCCACCCAGCGCGCGCGCGAGTCTCT 1122
Qy      232 -----ProGlyLeuProAlaAla----- 237
Db      1123 GCTGCTGCGGGCGGGAGCGGAGGGGGCGGGGAGACCCGGAGCGCGCGCGCT 1182
Qy      238 ---ProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArg 256
Db      1183 CTTCGCCGCGCGC--GCCCGCGCGCGCGCGCATGCTACGGGTACG--CCCCACGGCT 1238
Qy      256 ngIuGlunArgAlaSerProAlaGlyLysPheSerSerPheAlaIleAspSerIle 276
Db      1239 GCGGCTACGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1289
Qy      276 uArgGlyProPheArgSerArgArg-----LeuArgAspThrAla 290
Db      1290 CCGCGGAGAGGGCGCGCGCGCGCGCGCGCGCTTCCACCGGACTCGCCCCCGCGCGC 1349
Qy      290 ogIyThrThrLeuGlnTrpGlyAlaAlaProCysProPro-----LeuProAla 307
Db      1350 CGGCACCGCAGCGGCGC--GGCGCGCGAGTGGCGCGGACCGGCTTGGGTACGGGCGC 1406
Qy      307 eProAlaLeuLeuPro-----AlaAlaProCysArgAlaLeuLeuProLeuGlyAla 325
Db      1407 ACCCGGCTCG--CGCGCGCGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1463
Qy      325 rGlyAlaGlyGlyProAlaArgLeuGlyAlaArgGluAla----- 338
Db      1464 -----GCCCGGGCGCTCAGCGCTGGCGCGCTCGCTTCCATCGAGACATCATGGG 1519
Qy      339 -----GluValProProThrAlaProProLeuLeuLeuAl 350
Db      1520 GGAGAGCTTGGCGCGCGCGCGCTGCGCGCGCGCGCGCGAGCGCGCGCGCTCAG 1579
Qy      350 aProLeuProAlaAlaAlaPro-----AlaLysProLeuArgGlyProAlaAla 368
Db      1580 GCGCTCG--CCTCGCGCTCGCGCGGTGGCGCGCGCGCGCGCGCGCGCGAGG 1638
Qy      368 yAlaHisLeuThrCysProLeuArgLeuProAlaAlaLeuGluAlaAlaLeu--Val 388
Db      1639 C-----TGGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1668
Qy      388 rGPro--GlyProHisLeuSerTrpPro 396
Db      1669 GGCGCGCGCTCACCGGATCCCTCGTGGCGG 1697

```

RESULT 12
US-10-172-118-1045

```

; Sequence 1045, Application US/10172118
; Publication No. US2003022437A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yundong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999

```

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; CURRENT APPLICATION NUMBER: US/10/172, 118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1045
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_004472
; DATABASE ENTRY DATE: 2001-06-18
; US-10-172-118-1045

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Alignment Scores:

Pred. No.:	3,12e-28	Length:	2487
Score:	488.50	Matches:	170
Percent Similarity:	47.56%	Conservative:	35
Best Local Similarity:	39.44%	Mismatches:	147
Query Match:	23.01%	Indels:	83
DB:	13	Gaps:	20

US-10-087-080-32 (1-402) x US-10-172-118-1045 (1-2487)

```

Qy      14 AspLysGlnGlySerAspLeuGlnGlyAlaGlyLysSerAspAlaProSerProLeuSer 33
Db      506 GAAGAGAGAGACACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 564
Qy      34 AlAlaGlyAspAspSerLeuGlySerAspGlyAspCysAlaAlaIysProSerAlaGly 53
Db      565 GCGCGCGCGCGCGCGCGCGCGCTGTAACGCGGGAGAGACAGACTGAGAGATCTGAGAGGA 624
Qy      54 GlyGlyAlaArg--AspThrGlnGlyAspGlyGlnGlnSerAlaGlyGlyProGlyAl 73
Db      625 GAGAGACGAGATGACATCTG--CTGGCCCGCGCTGCGGGCGCGCGCGCGCGCGCG 678
Qy      73 agIuGlunAlaIleProAlaAlaAlaAlaAlaAlaAlaIleAlaGlyAlaGluAla 93
Db      679 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Qy      93 yAlaAlaGlyProGlyAlaGlyAlaGlySer---GlyGluGlyAlaArgSerTrp 112
Db      721 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 777
Qy      112 cTyThrArgArgProLysProProTyTrpSerTrpIleAlaLeuIleAlaMetAlaIle 132
Db      778 GCTGTG-----AAGCGCGCTTACTGTATATCGGCTCATCATGAGCCATCTCT 828
Qy      132 gaSPSerAlaGlyGlyArgLeuThrLeuAlaGluIleAsnGlyTrpLeuMetGlyLysPh 152
Db      829 GCAGAGCCCCAAGAGCGGTGACGCTGACGAGATCTGTGAGTTATCATCGGCGCGCTT 888
Qy      829 gAspSerAlaGlySerTrpThrGlyTrpArgAsnSerValArgHisAsnLeuSerIle 172
Db      152 eProPhePheArgGlySerTrpThrGlyTrpArgAsnSerValArgHisAsnLeuSerIle 172
Qy      889 CCCCCTACTACGGGAGAGATTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 948
Db      172 uasaspCysPheValIysValLeuArgAspProSerArgProTrpGlyLysAspArg 192
Qy      949 CAAAGCTGCTTCTCAAGATCCCCCGAGACCCGGCAACCGG--GGCAAGGGCAACTA 1005
Db      192 rTTPMeLeuAsnProAsnSerGlyThrPheAlaAspGlyValPheArgArgArg 212
Qy      1006 CTGGACCTGGACCCGGAGTCCGCCGACATGTTGACACAGCGAGCTTCTCGGCCGGAG 1065
Db      212 glyArgLeuSerHisArgAlaProValProAlaProGlyLeuArgProGluAla-- 231
Qy      1066 GAAGCGCTTCAAG--CGGACGCGCTGCTCCACCCAGCGCGCGCGCGCGAGTCTCT 1122
Db      232 -----ProGlyLeuProAlaAla----- 237
Qy      1123 GCTGCTGCGGGCGGGAGCGGAGGGGGCGGGGAGACCCGGAGCGCGCGCT 1182
Db      238 ---ProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArg 256

```



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Db      1290 CGCGCCGAGCGCGCGCGCGCGCGCGCTTCACCCGCACTGCGCCCGCGCGCC 1349
QY      290 oGlyThrThrLeuGlnTrpGlyAlaAlaProCysProPro-----LeuProAlaPh 307
Db      1350 CGCCACCGCAGCGCGC-----GGCGCGCAGCTGGCGCCGAGCCGCTTCGCTACCGGCGCG 1406
QY      307 eProAlaLeuLeuPro-----AlaAlaProCysArgAlaLeuLeuProLeuGlyAla 325
Db      1407 ACCCGCTCG-GCGCGCGCCCTACCGCGCCCTTCGCGCTCCCGCGCCAGGCGGCG-- 1463
QY      325 rGlyAlaGlyGluProAlaArgLeuGlyAlaArgAla----- 338
Db      1464 ----GCCCGCGCGCTCAGCGCTGCGCGCTCGCCCTTCACATCAGAGCATCATCGGG 1519
QY      339 -----GluValProProThrAlaProProLeuLeuLeuAl 350
Db      1520 GGCAGCTTGGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCTTCAG 1579
QY      350 aProLeuProAlaAlaAlaPro-----AlaCysProLeuArgGlyProAlaAlaGly 368
Db      1580 GCGCTCG-CCCTCGCCCTCGCGCGCTGGCGCGCGCGCGCGCATCCAGCGGAGAGG 1638
QY      368 yAlaHisLeuYrCysProLeuArgLeuProAlaAlaLeuGlnAlaAlaLeu-ValArgA 388
Db      1639 C-----TCGCGCGCGCGCAGCGCGCGCTGGCGCGCG 1668
QY      388 rGPro---GlyProHisLeuSerYrPro 396
Db      1669 GGCGCGCGCTCAGCCGATCCCTCGTGGCGG 1697

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RESULT 14

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US-09-968-007A-802
; Sequence 802, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Eber, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968, 007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 802
; LENGTH: 5181
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-802

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Alignment Scores:

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Pred. No.:      6,16e-28      Length:      5181
Score:          488.50      Matches:      170
Percent Similarity: 47.56%      Conservative: 35
Best Local Similarity: 39.44%      Mismatches: 147
Query Match:      23.01%      Indels:      83
Db:              12      Gaps:      20

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US-10-087-080-32 (1-402) x US-09-968-007A-802 (1-5181)

QY 14 AspGlyGlnGlySerAspLeuGlnGlyAlaGlyGlySerAspAlaProSerProLeuSer 33

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Db      2779 GAAGAGAGAGACGACGACGAGGGCGCGGATGGCGGCGC-CCGCTGTGCTGTCCCGCGCA 2837
QY      34 AlaAlaGlyAspAspSerLeuGlySerAspGlyAspCysAlaAlaAlaProSerAlaGly 53
Db      2838 GCGCGCGCGCGCGCGCGCTCGTACCGCGCGGAGCAGAGCTGAGATCTGAGAGAGGA 2897
QY      54 GylGlyAlaArg-AspThrGlnGlyAspGlyGlnGlnSerAlaGlyGlyGlyProGlyAl 73
Db      2898 GAGAGCAGAGATGACATCTG-----CTGGCCCCGCTGCTGGGGGCTCCCGCGCGC 2951
QY      73 aGlnGlnAlaLeuProAlaAlaAlaAlaAlaValAlaGlnGlyAlaGlnAlaGly 93
Db      2952 CCGCGCGCGCGCGCGCGCGCGCGCA-----GAGCGCGTGGGGG 2993
QY      93 yAlaAlaGlyProGlyAlaGlyGlyAlaGlySer---GlyGlnGlyAlaArgSerYr 112
Db      2994 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAAGAAC--CC 3050
QY      112 oTyThrArgArgProLysProProThrSerYrTrpAlaLeuLeuAlaMetAlaLeu 132
Db      3051 GCTGGTG-----AAGCGCCCTACTGTTATGCGCTCATCATATGCGCATCT 3101
QY      132 gAspSerAlaGlyGlyArgLeuThrLeuAlaGlnLeuGlnGlnGlnGlnGlnGlnGln 152
Db      3102 GCAGAGCCCCAGAGAGCGCTGACGCTGAGCGAGATCTGTGATTGATCAGCGCGCGCT 3161
QY      152 eProPhePheArgGlySerYrThrGlyTrpArgAsnSerValArgHisAsnLeuSer 172
Db      3162 CCCCTACTACCCGAGAGAGTTCCCGCGCGCGCGCGCGAGAGACAGCATCCGCGACAACTCGCT 3221
QY      172 uAsnAspCysPheValLeuValLeuArgAspProSerArgProTrpGlyLysAspAsn 192
Db      3222 CAGAGCTGCTTGTGTAAGATCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3278
QY      192 rTrpMetLeuAsnProAsnSerGlnYrThrPheAlaAspGlyValPheArgArgArg 212
Db      3279 CTGGAGCGTGGAGCCCGGAGATCCCGCGCGAGATGTTGCAACAGGAGGAGCTTCGCGCGGAG 3338
QY      212 GlySerGlnSerHisArgAlaProValProAlaProGlyLeuArgProGlnGlnAla 231
Db      3339 GAAGCGCTTCAAG---CGCGAGCGCGCTGCTCCCGCGCGCGCGCGCGCGCGCGCGCT 3395
QY      232 -----ProGlyLeuProAlaAla----- 237
Db      3396 GCTGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3455
QY      238 ---ProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArg 256
Db      3456 CTTCGCGCGCGCG- GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3511
QY      256 nGlnGlnArgAlaSerProAlaGlyLysPheSerSerSerPheAlaHisAspSerLeu 276
Db      3512 GCGGCTACGCGCTGCGCTGCG-----GCTTACGCGCGCGCGCTGCGCGCTTCTG 3562
QY      276 uArgLysProPheArgSerArgArg-----LeuArgAspThrAlaPro 290
Db      3563 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3622
QY      290 oGlyThrThrLeuGlnTrpGlyAlaAlaProCysProPro-----LeuProAlaPh 307
Db      3623 CGCCACCGCAGCGCGC-----GGCGCGCAGAGCTGCGCGCGCGCGCTTCGCTACCGCGCGC 3679
QY      307 eProAlaLeuLeuPro-----AlaAlaProCysArgAlaLeuLeuProLeuGlyAla 325
Db      3680 ACCCGCTCG-GCGCGCGCCCTACCGCGCCCTTCGCGCTCCCGCGCCAGGCGGCGG-- 3736
QY      325 rGlyAlaGlyGluProAlaArgLeuGlyAlaArgAla----- 338
Db      3737 ----GCCCGCGCGCTCAGCGCTGCGCGCTGCGCTTCATTCAGAGCATCATCGGG 3792
QY      339 -----GluValProProThrAlaProProLeuLeuLeuAl 350

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Wed Sep 8 12:04:29 2004

us-10-087-080-32.rnpb

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Search completed: September 2, 2004, 18:14:19
Job time : 611 secs
